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<b>(21) International Application Number:</b> PCT/GB97/01471 <b>(22) International Filing Date:</b> 30 May 1997 (30.05.97)  <b>(30) Priority Data:</b> 9611460.8 1 June 1996 (01.06.96) GB  <b>(71) Applicant (for all designated States except US):</b> LUDWIG INSTITUTE FOR CANCER RESEARCH [CH/CH]; Postfach, CH-8024 Zurich (CH).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> VANHASEBROECK, Bart [GB/GB]; Ludwig Institute for Cancer Research, Courtaul Building, 91 Riding House Street, London W1P 8BT (GB). WATERFIELD, Michael, Derek [GB/GB]; Ludwig Institute for Cancer Research, Courtaul Building, 91 Riding House Street, London W1P 8BT (GB).  <b>(74) Agent:</b> WILLIAM JONES LIMITED; The Crescent, 54 Blossom Street, York YO2 2AP (GB).		<b>(81) Designated States:</b> AU, CA, CN, JP, KR, NZ, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).  <b>Published</b> <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
<b>(54) Title:</b> LIPID KINASE  <b>(57) Abstract</b>  The invention relates to a novel lipid kinase which is part of the PI3 Kinase family. PI3 Kinases catalyse the addition of phosphate to inositol generating inositol mono, di and triphosphate. Inositol phosphates have been implicated in regulating intracellular signalling cascades resulting in alternations in gene expression which, amongst other effects, can result in cytoskeletal remodelling and modulation of cellular motility. More particularly the invention relates to a novel human PI3 Kinase, p110 $\delta$ which interacts with p85, has a broad phosphoinositide specificity and is sensitive to the same kinase inhibitors as PI3 Kinase p110 $\alpha$ . However in contrast to previously identified PI3 Kinases which show a ubiquitous pattern of expression, p110 $\delta$ is selectively expressed in leucocytes. Importantly, p110 $\delta$ shows enhanced expression in most melanomas tested and therefore may play a crucial role in regulating the metastatic property exhibited by melanomas. The identification of agents that enhance or reduce p110 $\delta$ activity may therefore prevent cancer metastasis.		

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## LIPID KINASE

The invention relates to a novel lipid kinase which is part of the PI3 Kinase (PI3K) family and more specifically the invention relates to various aspects  
5 of the novel lipid kinase particularly, but not exclusively, to an identification of expression of said kinase with a view to diagnosing or predicting motility or invasion of cells such as metastasis of cancer cells; and also agents for interfering with said expression or inhibiting said kinase with a view to enhancing or reducing or preventing said motility or invasion so as to  
10 enhance or restrict, respectively the movement of selected cells.

An overview of the PI3 kinase family of enzymes is given in our co-pending Patent Application WO93/21328. Briefly, this class of enzymes shows phosphoinositide (hereinafter referred to after as PI) 3-kinase activity. Following major advances in our knowledge of cell signal transduction and  
15 cell second messenger systems it is known that the PI3Ks have a major role to play in regulating cell function. Indeed, it is known that PI3Ks are members of a growing number of potential signalling proteins which associate with protein-tyrosine kinases activated either by ligand stimulation or as a consequence of cell transformation. Once thus associated they provide an  
20 important complex in the cell signalling pathway and thus direct events towards a given conclusion.

PI3 kinases catalyse the addition of phosphate to the 3'-OH position of the inositol ring of inositol lipids generating phosphatidyl inositol monophosphate, phosphatidyl inositol diphosphate and phosphatidyl inositol  
25 triphosphate (Whitman et al, 1988, Stephens et al 1989 and 1991). A family

of PI3 kinase enzymes has now been identified in organisms as diverse as plants, slime molds, yeast, fruit flies and mammals (Zvelebil et al, 1996).

It is conceivable that different PI3 kinases are responsible for the generation of the different 3'-phosphorylated inositol lipids *in vivo*. Three classes of PI3  
5 kinase can be discriminated on the basis of their *in vitro* lipid substrates specificity. Enzymes of a first class have a broad substrate specificity and phosphorylate PtdIns, PtdIns(4)P and PtdIns(4,5)P<sub>2</sub>. Class I PI3 kinases include mammalian p110 $\alpha$ , p110 $\beta$  and p110 $\gamma$  (Hiles et al, 1992; Hu et al, 1993; Stephens et al, 1994; Stoyanov et al, 1995).

10 P110 $\alpha$  and p110 $\beta$  are closely related PI3 kinases which interact with p85 adaptor proteins and with GTP-bound Ras.

Two 85 kDa subunits, p85 $\alpha$  and p85 $\beta$ , have been cloned (Otsu et al, 1992). These molecules contain an N-terminal *src* homology-3 (SH3) domain, a breakpoint cluster (bcr) homology region flanked by two proline-rich regions  
15 and two *src* homology-2 (SH2) domains. Shortened p85 proteins, generated by alternative splicing from the p85 $\alpha$  gene or encoded by genes different from those of p85 $\alpha/\beta$ , all lack the SH3 domain and the bcr region, which seem to be replaced by a unique short N-terminus (Pons et al, 1995; Inukai et al, 1996; Antonetti et al, 1996). The SH2 domains, present in all p85  
20 molecules, provide the heterodimeric p85/p110 PI3Ks with the capacity to interact with phosphorylated tyrosine residues on a variety of receptors and other cellular proteins. In contrast to p110 $\alpha$  and  $\beta$ , p110 $\gamma$  does not interact with p85 but instead associates with a p101 adaptor protein (Stephens et al, 1996). P110 $\gamma$  activity is stimulated by G-protein subunits.

PI3Ks of a second class contains enzymes which, at least *in vitro*, phosphorylate PtdIns and PtdIns(4)P but not PtdIns(4, 5)P<sub>2</sub> (MacDougall et al, 1995; Virbasius et al, 1996, Molz et al, 1996). These PI3Ks all contain a C2 domain at their C-terminus. The *in vivo* role of these class II PI3Ks is unknown.

A third class of PI3K has a substrate specificity restricted to PtdIns. These PI3Ks are homologous to yeast Vps34p which is involved in trafficking of newly formed proteins from the Golgi apparatus to the vacuole in yeast, the equivalent of the mammalian lysosome (Stack et al, 1995). Both yeast and mammalian Vps34p occur in a complex with Vps15p, a 150 kDa protein serine/threonine kinase (Stack et al, 1995; Volinia et al, 1995; Panaretou et al, submitted for publication).

PtdIns(3)P is constitutively present in cells and its levels are largely unaltered upon extracellular stimulation. In contrast, PtdIns(3, 4)P<sub>2</sub> and PtdIns(3, 4, 5)P<sub>3</sub> are almost absent in quiescent cells but are produced rapidly upon stimulation by a variety of growth factors, suggesting a likely function as second messengers (Stephens et al, 1993). The role of PI3Ks and their phosphorylated lipids in cellular physiology is just beginning to be understood. These lipids may fulfill a dual role: apart from exerting physical, charge-mediated effects on the curvature of the lipid bilayer, they also have the capacity to interact with specific binding proteins and modulate their localisation and/or activity. Amongst the potential targets for these lipids are protein kinases such as protein kinase C isoforms, protein kinase N/Rho-activated kinases and Akt/RAC/protein kinase B (Toker et al, 1994; Palmer et al, 1995; Burgering and Coffey, 1995; Franke et al, 1995; James et al, 1996; Klippel et al, 1996). Akt/RAC/protein kinase B is likely to be

upstream of targets such as p70 S6 kinase and glycogen synthase kinase-3 (Chung et al, 1994; Cross et al, 1995). PI3Ks also affect the activity of small GTP-binding proteins such as Rac and Rab5, possibly by regulating nucleotide exchange (Hawkins et al, 1995; Li et al, 1996). Ultimately, the combination of these actions can result in cytoskeletal rearrangements, DNA synthesis/mitogenesis, cell survival and differentiation (Vanhaesebroeck et al, 1996).

We describe herein a mammalian novel Class I PI3 Kinase which we have termed p110 $\delta$ . This novel PI3 Kinase typifies the Class I PI3 Kinase family in that it binds p85 $\alpha$ , p85 $\beta$  and p85 $\gamma$ . In addition, it also binds GTP-ras but, like p110 $\alpha$ , shows no binding of rho and rac. It also shares the same GTP-broad phosphoinositide lipid substrate specificity of p110 $\alpha$  and p110 $\beta$ , and it also shows protein kinase activity and has a similar drug sensitivity to p110 $\alpha$ .

However, it is characterised by its selective tissue distribution. In contrast to p110 $\alpha$  and p110 $\beta$  which seem to be ubiquitously expressed, p110 $\delta$  expression is particularly high in white blood cell populations i.e. spleen, thymus and especially peripheral blood leucocytes. In addition to this observation we have also found that p110 $\delta$  is expressed in most melanomas, but not in any melanocytes, the normal cell counterpart of melanomas. Given the natural distribution of p110 $\delta$  in tissues which are known to exhibit motility or invasion and also the expression of p110 $\delta$  in cancer cells we consider that p110 $\delta$  has a role to play in cell motility or invasion and thus the expression of this lipid kinase in cancer cells can explain the metastatic behaviour of cancer cells.

A further novel feature of p110 $\delta$  is its ability to autophosphorylate in a Mn<sup>2+</sup> - dependent manner. Indeed, we have shown that autophosphorylation tends to hinder the lipid kinase activity of the protein. In addition, p110 $\delta$  contains distinct potential protein:protein interaction modules including a proline-rich region (see Figure 1, position 292-311, wherein 8 out of 20 amino acids are proline) and a basic region leucine zipper (bZIP) like domain (Ing et al., 1994 and Hirai et al., 1996). Such biochemical and structural differences between p85-binding PI3 kinases indicate that they may fulfill distinct functional roles and/or be differentially regulated *in vivo*.

We disclose herein a nucleic acid molecule, of human origin, and corresponding amino acid sequence data relating to p110 $\delta$ . Using this information it is possible to determine the expression of p110 $\delta$  in various tissue types and in particular to determine the expression of same in cancer tissue with a view to diagnosing the motility or invasiveness of such tissue and thus predicting the potential for secondary tumours occurring. Moreover, it will also be possible to provide agents which impair the expression of p110 $\delta$  or alternatively interfere with the functioning of same. For example, having regard to the sequence data provided herein it is possible to provide antisense material which prevents the expression of p110 $\delta$ .

As mentioned above, the invention embraces antisense oligonucleotides that selectively bind to a nucleic acid molecule encoding a PI3K $\delta$  protein, to decrease transcription and/or translation of PI3K $\delta$  genes. This is desirable in virtually any medical condition wherein a reduction in PI3K $\delta$  gene product expression is desirable, including to reduce any aspect of a tumor cell phenotype attributable to PI3K $\delta$  gene expression. Antisense molecules, in this manner, can be used to slow down or arrest such aspects of a tumor cell

phenotype.

As used herein, the term "antisense oligonucleotide" or "antisense" describes an oligonucleotide that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and thereby, inhibits the transcription of that gene and/or the translation of that mRNA. The antisense molecules are designed so as to interfere with transcription or translation of a target gene upon hybridization with the target gene. Those skilled in the art will recognize that the exact length of the antisense oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise that sequence. It is preferred that the antisense oligonucleotide be constructed and arranged so as to bind selectively with the target under physiological conditions, i.e., to hybridize substantially more to the target sequence than to any other sequence in the target cell under physiological conditions. Based upon the DNA sequence presented in Figure 9 or upon allelic or homologous genomic and/or DNA sequences, one of skill in the art can easily choose and synthesize any of a number of appropriate antisense molecules for use in accordance with the present invention. In order to be sufficiently selective and potent for inhibition, such antisense oligonucleotides should comprise at least 7 (Wagner et al., *Nature Biotechnology* 14:840-844, 1996) and, more preferably, at least 15 consecutive bases which are complementary to the target. Most preferably, the antisense oligonucleotides comprise a complementary sequence of 20-30 bases. Although oligonucleotides may be chosen which are antisense to any region of the gene or mRNA transcripts, in preferred embodiments the



antisense oligonucleotides correspond to N-terminal or 5' upstream sites such as translation initiation, transcription initiation or promoter sites. In addition, 3'-untranslated regions may be targeted. Targeting to mRNA splicing sites has also been used in the art but may be less preferred if alternative mRNA splicing occurs. In addition, the antisense is targeted, preferably, to sites in which mRNA secondary structure is not expected (see, e.g., Sainio et al., *Cell Mol. Neurobiol.* 14(5):439-457. 1994) and at which proteins are not expected to bind. Finally, although Figure 9 discloses cDNA sequence, one of ordinary skill in the art may easily derive the genomic DNA corresponding to the cDNA of Figure 9. Thus, the present invention also provides for antisense oligonucleotides which are complementary to the genomic DNA corresponding to Figure 9. Similarly, antisense to allelic or homologous DNAs and genomic DNAs are enabled without undue experimentation.

In one set of embodiments, the antisense oligonucleotides of the invention may be composed of "natural" deoxyribonucleotides, ribonucleotides, or any combination thereof. That is, the 5' end of one native nucleotide and the 3' end of another native nucleotide may be covalently linked, as in natural systems, via a phosphodiester internucleoside linkage. These oligonucleotides may be prepared by art recognized methods which may be carried out manually or by an automated synthesizer. They also may be produced recombinantly by vectors.

In preferred embodiments, however, the antisense oligonucleotides of the invention also may include "modified" oligonucleotides. That is, the oligonucleotides may be modified in a number of ways which do not prevent them from hybridizing to their target but which enhance their stability or targeting or which otherwise enhance their therapeutic effectiveness.

The term "modified oligonucleotide" as used herein describes an oligonucleotide in which (1) at least two of its nucleotides are covalently linked via a synthetic internucleoside linkage (i.e., a linkage other than a phosphodiester linkage between the 5' end of one nucleotide and the 3' end of another nucleotide) and/or (2) a chemical group not normally associated with nucleic acids has been covalently attached to the oligonucleotide. Preferred synthetic internucleoside linkages are phosphorothioates, alkylphosphonates, phosphorodithioates, phosphate esters, alkylphosphonothioates, phosphoramidates, carbamates, phosphate triesters, acetamides, peptides, and carboxymethyl esters.

The term "modified oligonucleotide" also encompasses oligonucleotides with a covalently modified base and/or sugar. For example, modified oligonucleotides include oligonucleotides having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified oligonucleotides may include a 2'-O-alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose instead of ribose. Modified oligonucleotides also can include base analogs such as C-5 propyne modified bases (Wagner et al., *Nature Biotechnology* 14:840-844, 1996). The present invention, thus, contemplates pharmaceutical preparations containing modified antisense molecules that are complementary to and hybridizable with, under physiological conditions, nucleic acids encoding PI3K $\delta$  proteins, together with pharmaceutically acceptable carriers.

Antisense oligonucleotides may be administered as part of a pharmaceutical composition. Such a pharmaceutical composition may include the antisense

oligonucleotides in combination with any standard physiologically and/or pharmaceutically acceptable carriers which are known in the art. The compositions should be sterile and contain a therapeutically effective amount of the antisense oligonucleotides in a unit of weight or volume suitable for administration to a patient. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. The term "physiologically acceptable" refers to a non-toxic material that is compatible with a biological system such as a cell, cell culture, tissue, or organism. The characteristics of the carrier will depend on the route of administration. Physiologically and pharmaceutically acceptable carriers include diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials which are well known in the art.

It is therefore an object of the invention to identify a novel PI3 Kinase and so provide means for predicting the likely motility or invasiveness of cells.

It is a yet further object of the invention to provide agents that enhance or reduce or prevent the expression of p110 $\delta$  and/or agents which interfere with the functioning of p110 $\delta$ , with a view to enhancing or hindering or preventing, respectively, the motility or invasiveness of cells.

According to a first aspect of the invention there is therefore provided an isolated autophosphorylating polypeptide which possesses PI3 kinase activity.

Ideally said polypeptide is derived from white blood cells and is typically expressed in melanomas, more ideally still said polypeptide is of human origin.

Moreover, the polypeptide is capable of association with p85 subunits of mammalian PI3 Kinases ideally to produce active complexes.

More preferably still the polypeptide has the amino acid sequence shown in Fig. 1A or a sequence homologous thereto which is in particularly characterised by a proline rich domain.

Reference herein to the term homologous is intended to cover material of a similar nature or of common descent or possessing those features, as herein described, that characterise the protein, or material, whose corresponding nucleic acid molecule hybridises, such as under stringent conditions, to the nucleic acid molecule shown in Figure 9. Typical hybridisation conditions would include 50% formamide, 5 X SSPE, 5 X Denhardt's solution, 0.2% SDS, 200 µg/ml denatured sonicated herring sperm DNA and 200 µg/ml yeast RNA at a temperature of 60°C, (conditions described in the published patent specification WO 93/21328).

Ideally the polypeptide is produced using recombinant technology and is typically of human origin.

According to a further aspect of the invention there is provided an antibody to at least a part of the polypeptide of the invention, which antibody may be polyclonal or monoclonal.

According to a further aspect of the invention there is provided the whole or a part of the nucleic acid molecule shown in Fig. 9 which molecule encodes an autophosphorylating polypeptide having PI3 Kinase activity.

In the instance where said part of said molecule is provided, the part will be selected having regard to its purpose, for example it may be desirable to select a part having kinase activity for subsequent use or another part which is most suitable for antibody production.

- 5 According to a further aspect of the invention there is provided a nucleic acid molecule construct comprising a whole or a part of the nucleic acid molecule of the invention wherein the latter nucleic acid molecule is under the control of a control sequence and in appropriate reading frame so as to ensure expression of the corresponding protein.
- 10 According to a yet further aspect of the invention there is provided host cells which have been transformed, ideally using the construct of the invention, so as to include a whole or a part of the nucleic acid molecule shown in Fig. 9 so as to permit expression of a whole, or a significant part, of the corresponding polypeptide.
- 15 Ideally these host cells are eukaryotic cells for example, insect cells such as cells from the species *Spodoptera frugiperda* using the baculovirus expression system. This expression system is favoured in the instance where post translation modification is required. If such modification is not required a prokaryotic system may be used.
- 20 According to a further aspect of the invention there is provided a method for diagnosing the motility of cells comprising examining a sample of said cells for the expression of the polypeptide of the invention.

Ideally, investigations are undertaken in order to establish whether mRNA

corresponding to the polypeptide of the invention is expressed in said cells, for e.g. by using PCR techniques or Northern Blot analysis. Alternatively, any other conventional technique may be undertaken in order to identify said expression.

- 5 According to a yet further aspect of the invention there is provided a method for identifying antagonists effective at blocking the activity of the polypeptide of the invention which comprises screening candidate molecules for such activity using the polypeptide, or fragments thereof the invention.

10 Ideally, screening may involve artificial techniques such as computer-aided techniques or conventional laboratory techniques.

Ideally, the above method is undertaken by exposing cells known to express the polypeptide of the invention, either naturally or by virtue of transfection, to the appropriate antagonist and then monitoring the motility of same.

- 15 Alternatively, the method of the invention may involve competitive binding assays in order to identify agents that selectively and ideally irreversibly bind to the polypeptide of the invention.

20 According to a yet further aspect of the invention there is provided a pharmaceutical or veterinary composition comprising an agent effective at enhancing or blocking the activity or expression of the polypeptide of the invention which has been formulated for pharmaceutical or veterinary use and which optionally also includes a dilutant, carrier or excipient and/or is in unit dosage form.

According to a yet further aspect of the invention there is provided a method for controlling the motility of cells comprising exposing a population of said cells to either an agonist or antagonist or the polypeptide of the invention or to antisense material as hereindescribed.

- 5      Alternatively, in the aforementioned method said cells may be exposed alternatively or additionally, to the polypeptide of the invention with a view to increasing the effective levels of said polypeptide and so enhancing cell motility.

The aforementioned method may be undertaken either *in vivo* or *in vitro*.

- 10     According to a yet further aspect of the invention there is provided use of an agent effective at blocking the activity of the polypeptide of the invention for controlling cell motility.

According to a yet further aspect of the invention there is provided use of the polypeptide of the invention for enhancing cell motility.

- 15     According to a yet further aspect of the invention there is provided antisense oligonucleotides ideally modified as hereindescribed, for hybridizing to the nucleic acid of the invention.

An embodiment of the invention will now be described by way of example only with reference to the following figures, materials and methods wherein:

- 20     Fig. 1(A) shows translated amino acid sequence of human p110 $\delta$  cDNA. The proline-rich region and the bZIP-like domain are indicated by open and

shaded box, respectively. (B) Dotplot comparison of the full length amino acid sequence of p110 $\delta$  with that of p110 $\alpha$  and p110 $\beta$ . Non-conserved sequence motifs are underlined. Dotplot comparisons were performed using the COMPARE program (UWGCG package: Devereux et al, 1984). (C) Comparison of the p110 $\delta$  amino acid sequence flanking HR3 with respective homologous regions of p110 $\alpha$  and p110 $\beta$ . Amino acid numbering is that of p110 $\delta$ . Proline-rich region: critical prolines enabling the formation of a left-handed polyproline type-II helix in p110 $\delta$  are indicated with an asterisk. bZIP region: conserved L/V/I residues of the leucine-zipper region are indicated with arrowheads.

Fig. 2. Interaction of p110 $\delta$  with p85 and Ras (A) Insect cells were infected with recombinant baculovirus encoding GST-p110 $\delta$ , alone or in combination with viruses encoding either p85 $\alpha$ ,  $\beta$  or  $\gamma$ . After 2 days, GST-p110 $\delta$  was affinity-purified from the cell lysates using glutathione-sepharose, washed, and analysed by SDS-PAGE and Coomassie staining. (B) P110 $\delta$  was immunoprecipitated from 500  $\mu$ g human neutrophil cytosol and probed for the presence of different p85 isoforms by Western blotting. rec = recombinant p85 purified from Sf9 cells. (C) GST-p110 $\alpha$ /85 $\alpha$  and GST-p110 $\delta$ /85 $\alpha$  (0.25  $\mu$ g) were incubated with the indicated amount (in  $\mu$ g) of GTP- or GDP-loaded V12-Ras, washed and probed for the presence of Ras by Western blotting as described (Rodriguez-Viciana et al, 1994, 1996).

Fig. 3. (A) *In vitro* lipid substrate specificity of p110 $\delta$ . GST-p110 $\delta$ /p85 $\alpha$  was used in a lipid kinase assay using the indicated substrates in the presence of Mg<sup>2+</sup>. Equal cpm were spotted at the origin. (B) HPLC analysis of the PtdIns phosphorylation product generated by GST-p110 $\delta$ /p85 $\alpha$ . Elution times of the deacylated product of p110 $\delta$  (solid line) and



glycerophosphoinositol-3P and glycerophosphoinositol-4P standards (dotted lines) are shown. The positions of the AMP and ADP controls are indicated by arrows.

Fig. 4. Protein kinase activity of p110 $\delta$ . (A) GST-p110 $\alpha$  or GST-p110 $\delta$ ,  
5 in complex with the indicated p85 subunits, were subjected to an *in vitro*  
protein kinase reaction in the presence of Mn<sup>2+</sup>, and further analysed by SDS-  
PAGE, Coomassie staining and autoradiography, (B,C) Untagged p110 $\alpha$  and  
p110 $\delta$  [wild-type (WT) or kinase defective mutants (p110 $\alpha$ -R916P and  
10 p110 $\delta$ -R894P)], in complex with p85 $\alpha$  or  $\beta$  on PDGF-receptor  
phosphopeptide beads, were subjected to an *in vitro* kinase reaction and  
further analysed as described under (A). Open and closed arrowheads point  
to p110 and p85 proteins, respectively. Right panel in (B): phosphoamino  
acid analysis of p85 $\alpha$  and p110 $\delta$ .

Fig. 5. Sensitivity of p110 $\delta$  lipid kinase activity to drugs. Inhibition of  
15 p110 $\delta$ /p85 $\alpha$  (closed circles) and p110 $\alpha$ /p85 $\alpha$  (open circles) is normalised to  
activity in the absence of the drug wortmannin. These data points are the  
mean ( $\pm$ SE) of 3 experiments.

Fig. 6. Northern blot analysis of expression of p110 $\alpha$ , p110 $\beta$  and p110 $\delta$ .

Fig. 7. Analysis of p110 $\alpha$  and p110 $\delta$  protein expression. 100 $\mu$ g of total cell  
20 lysate was loaded per lane. Platelets were lysed in either lysis buffer as  
described under Materials and Methods, or in Laemmli gel loading buffer  
containing 2-mercaptoethanol. PMBC, peripheral blood mononuclear cells;  
PBL, peripheral blood lymphocytes.

Fig. 8. Involvement of p110 $\alpha$  and p110 $\delta$  in cytokine signalling. Ba/F3 (A) and MC/9 (B) cell lines were stimulated with the indicated cytokines. Samples from control untreated cells are labelled Con. Total cell lysates, and p110 $\alpha$  and p110 $\delta$  IPs were separated by SDS-PAGE to prepare duplicate blots, the references for which were p110 $\delta$ /85 $\alpha$  (panels a, b and d) or p110 $\alpha$ /85 $\alpha$  (panels c and e). Immunoblotting of native blots were performed with 4G10 (anti-PTyr, panels a) and anti-p110 $\alpha$  (panels c). Blots were subsequently stripped and reprobed with anti-SHP2. (A, panel b), anti-kit (B, panel b), anti-p110 $\delta$  (panels d) and anti-p85 antibodies (panels e). The arrowheads indicate the positions of p170 (IRS-2), p100 and p70 (SHP2) (A, panel a), and of p150 (c-kit) and p100 (B, panel b).

Fig. 9. The complete human cDNA sequence of p110 $\delta$ .

Fig. 10. Represents immunofluorescence images of murine macrophages microinjected with affinity purified antibodies to p110 $\delta$ . The macrophage cytoskeletons are imaged with phalloidin conjugated rhodamine.

## MATERIALS AND METHODS

### Cloning of p110 $\delta$

Details of the isolation of partial PI3 kinase cDNA clones via RT-PCR based on homologous regions between bovine p110 $\alpha$  and *S. cerevisiae* Vps34p have been described (Volinia *et al.*, 1995; MacDougall *et al.*, 1996). This approach yielded from the MOLT4 T cell line a partial p110 $\delta$  cDNA fragment which was then used to screen an oligo(dT)-primed U937 cDNA library (Volinia *et al.*, 1995). Complementary DNA was EcoRI-XhoI cloned

in Lambda ZAPII vector digested with EcoRI-XhoI (Stratagene). Out of 4 million clones screened, 6 primary positive plaques were found, 3 of which remained positive during two further rounds of screening. The cDNA inserts in pBluescript were prepared by *in vivo* excision according to the manufacturer's (Stratagene) instructions. Three representative pBluescript clones ( $O_{5.1}$ ,  $O_{9.1}$  and  $O_{11.1}$ ) were characterised by restriction mapping and PCR, and found to contain inserts with sizes ranging from 4.4 kb ( $O_{11.1}$ ) to 5.0 kb ( $O_{5.1}$ ,  $O_{9.1}$ ). Clone  $O_{9.1}$  was used for detailed characterisation. Restriction mapping of its insert revealed the absence of an internal XhoI site, and the presence of 2 internal EcoRI sites, respectively 223 and 3862 nucleotides 3' from the EcoRI cDNA insertion site (nucleotide 1 = underlined nucleotide of Figure 9). Consequently, combined EcoRI and XhoI digest divided the  $O_{9.1}$  insert in 3 fragments, further indicated as EcoRI fragment I (nucleotide 1-222), EcoRI fragment II (nucleotide 223-3861) and EcoRI-XhoI fragment III (nucleotide 3862-5000 approximately). Both strands of fragments I and II were sequenced using the Taq DyeDeoxy Terminator Cycle sequencing system (ABI) and the complete cDNA sequence is shown in Fig. 9. An open reading frame spanning nucleotides 195 to 3330 of the  $O_{9.1}$  insert was found. An in frame stop codon precedes the potential start codon, which lies in a favourable context for translation initiation (Kozak, 1991). This results in 196 nucleotides of 5' untranslated region (UT) and approximately 2.2 kb 3' UT. In the sequenced 5' end of  $O_{5.1}$ ,  $O_{9.1}$  and  $O_{11.1}$  clones, 2 different but related 5' untranslated regions were found indicative for the existence of at least 2 slightly different messenger RNAs.

## 25 Construction of expression vectors for p110 $\delta$

Insect cell transfer vectors used were pVL1393 (for untagged p110 $\delta$ ;

InVitrogen) and pAcG3X (for GST-p110 $\delta$ ; Davies et al., 1993). The coding region for p110 $\delta$  was subcloned in these vectors in two steps. First, the expression vectors were engineered, via linker insertion at the multicloning site, to contain part of the sequence of EcoRI fragment I of p110 $\delta$ , spanning  
5 the start codon (at nucleotide 197; see above) to the second EcoRI site (nucleotide 223; see above). In the latter EcoRI site, EcoRI fragment II of p110 $\delta$  was subcloned, followed by selection for clones with correctly orientated inserts. The first step for the insect cell vectors was BamHI-EcoRI cleavage followed by insertion of the following linker (linker I):

10 GATCCCCACCATGCCCCCTGGGGTGGACTGCCCCATGG (sense: 5'-3')  
(antisense: 5'-3') AATTCCATGGGGCAGTCCACCCCAGGGGGCATGGTGGG

This linker contains the ATG with an optimal Kozak consensus sequence (Kozak, 1991). Further derivatives of p110 $\delta$  were made by PCR using Vent DNA polymerase (New England Biolabs). P110 $\delta$  EcoRI fragment II, subcloned in pBluescript-SK (further indicated as pBluescript-p110 $\delta$ -EcoII)  
15 was hereby used as a template. In these PCR reactions, the 3'-untranslated region of the EcoRI fragment II insert was removed. Oligonucleotides used to create the mutation R894P were as follows: sense mutagenic oligonucleotide = PRIMER 1 (mutagenic residue underlined) =

20 5'-GTGTGGCCACATATGTGCTGGGCATTGGCGATCCGCACAGCGACA  
ACATCATGATCCG,

Anti-sense = PRIMER 2 =

5'-GGCCCGGTGCTCGAGAATTCTACTGCCTGTTGTCTTTGGACACGT

TGTGGGCC.

A parallel PCR was performed using primer 2, and a sense primer (PRIMER 3 = 5' - GTGTGGCCACATATGTGCTGGGCATTGGCG) leaving the wild type p110 $\delta$  sequence intact. All PCR products were cleaved with NdeI and XhoI, subcloned into NdeI-XhoI-opened pBluescript-p110 $\delta$ -EcoII and sequenced. Correct clones were then transferred as an EcoRI cassette into EcoRI-opened pVL1393 containing linker I followed by selection for clones with correctly orientated insert.

### Expression of p110 $\delta$ in insect cells

Plasmid DNA was cotransfected with BaculoGold DNA (Pharmingen, San Diego, CA) using Lipofectin reagent (Gibco). Recombinant plaques were isolated and characterised by established methods (Summers and Smith, 1987).

### Cell Culture

Cells were cultured in a humidified 5% CO<sub>2</sub> incubator in RPMI 1640 medium supplemented with 10% fetal bovine serum, 20  $\mu$ M 2-mercaptoethanol, 100 units/ml penicillin/streptomycin and 2 mM glutamine. Ba/F3 is a murine IL3-dependent pre-B cell line (Palacios and Steinmetz, 1985) and MC/9 is a murine IL3-dependent mast cell line (Nabel *et al.*, 1981). Both Ba/F3 and MC/9 were maintained in 10% (v/v) conditioned medium derived from WEHI3B, as the source of murine IL3. FDMAC11/4.6 (FD-6) myeloid progenitor cells are an indigenous variant of FDMAC11 which will grow in response to IL4, as well as IL3, GM-CSF and CSF-1 (Welham *et al.*, 1994a).

These cells were maintained in 3% (v/v) IL4-conditioned medium derived from the AgX63/OMIL4 cells (Karasuyama and Melchers, 1988).

### Lipid Kinase assay

Lipid kinase activity was performed essentially as described by Whitman *et al.* (1985). Lipid kinase assay buffer was 20 mM Tris HCl pH 7.4, 100 mM NaCl and 0.5 mM EGTA. Lipids were purchased from Sigma. The final concentration of ATP and  $Mg^{2+}$  in the assay were routinely 0.5 and 3.5 mM, respectively, while lipids were used at 0.2-0.4 mM concentration. Unless otherwise indicated, kinase reaction was for 10 min at 37°C. The solvent for TLC separation of reaction products was propan-1-ol/2 M acetic acid/5 M  $H_3PO_4$  (65:35:1). Assays of drug effects on the kinase were performed using PtdIns as substrate in the presence of 40  $\mu$ M ATP (final) for 10 min at 25°C; all tubes contained 1% DMSO. Activity was quantified by phosphorimager (Molecular Dynamics) analysis of TLC-separated lipid products.

### HPLC analysis

$[^{32}P]$ -PtdIns3P, prepared by phosphorylating PtdIns with recombinant p110 $\alpha$ , and  $[^{32}P]$ -PtdIns4P, generated by converting PtdIns with A431 membranes in the presence of 0.5% NP-40, were used as standards. Glycerophosphoinositols, generated by deacylation of lipids with methylamine (Clarke and Dawson, 1981), were separated by anion exchange HPLC on a PartisphereSAX column (Whatman International) using a linear gradient of 1 M  $(NH_4)_2HPO_4$  against water (0-25% B; 60 min) at 1ml/min. Radioactive peaks were detected by an on-line detector (Reeve Analytical, Glasgow).

ADP and ATP nucleotide standards, added as internal controls to ensure consistency between runs, were detected by absorbance at 254nm.

### ***In vitro* protein phosphorylation assay and effect on lipid kinase activity**

Precipitated proteins were incubated for 30 min at 37°C in protein kinase  
5 assay buffer (20 mM Tris.HCl (pH 7.4), 100 mM NaCl, 0.5 mM EGTA, 50  
μM ATP and 1 mM MnCl<sub>2</sub>.4H<sub>2</sub>O, 5-10 μCi[ γ-<sup>32</sup>P]ATP/ml). The reaction  
was stopped by addition of SDS-PAGE sample buffer, and the reaction  
products analysed by SDS-PAGE and autoradiography. Phosphoamino acid  
analysis was performed on a Hunter thin layer electrophoresis system (CBS  
10 Scientific Co, Del Mar, CA) as described (Jelinek and Weber, 1993).

### **Interaction of small GTP-binding proteins with PI-3K *in vitro***

Binding of ras, rac and rho to GST-PI3K was performed as described  
(Rodriguez-Viciana *et al.*, 1995, 1996).

### **Antibodies, immunoprecipitations and immunoblotting**

15 Monoclonal antibodies to bovine p85α (U1, U13), and p85β (T15) have been  
described (End *et al.*, Reif *et al.*, 1993). A monoclonal antibody (I2) against  
bovine p85γ was developed in our laboratory. Rabbit polyclonal antiserum  
against GST-human p85α (AA 5-321) was kindly provided by Dr. P.  
Shepherd, University College London. Rabbit polyclonal antisera were raised  
20 against a C-terminal peptide of p110δ (C)KVNWLAHNVSKDNRQ<sub>1044</sub> and  
against an N-terminal peptide of human p110α  
(CGG)SVTQEAEEREFFDETRR<sub>88</sub>. To raise antibodies directed against the

phosphorylated form of p110 $\delta$ , the peptide sequence 1044 was phosphorylated at the serine residue during peptide synthesis. An antiserum to the C-terminus of human p110 $\alpha$  (KMDWIFHTIKQHALN) was kindly provided by Dr. Roya Hooshmand-Rad (Ludwig Institute for Cancer Research, Uppsala, Sweden). Antibodies were affinity-purified on peptides coupled to Actigel (Sterogene Bioseparations, Arcadia, CA) or to AF-Amino ToyoPearl TSK gel (Tosho Co, Japan). Antibodies were found to be specific for the PI3K to which they were directed (tested against the following panel of PI-3K, expressed in Sf9 cells: bovine p110 $\alpha$ , human p110 $\beta$  (C. Panaretou and R.S.; unpublished results), human p110 $\gamma$  (Stoyanov *et al.*, 1995), p110 $\delta$ , PI-specific 3 -kinase (Volinia *et al.*, 1995). Peripheral blood cells were purified over a ficoll gradient (Lymphoprep; Nycomed, Oslo, Norway). Neutrophil cytosol was prepared by sonication as described (Wientjes *et al.*, 1993). Lysis buffer was 1% Triton-X100, 150 mM NaCl, 1 mM EDTA, 1 mM NaF, 1 mM NaVO<sub>3</sub>, 1 mM DTT, 1 mM PMSF, 0.27 TIU/ml aprotinin and 10  $\mu$ M leupeptin. In some experiments, 1mM disopropylfluorophosphate and 27 mM Na-p-tosyl-L-lysine chloromethyl ketone (hydrochloride) were added. Lysis buffer used for cytokine experiments was 50 mM Tris.HCl, pH 7.5, 10% (v/v) glycerol, 1% (v/v) NP-40, 150 mM NaCl, 100  $\mu$ M sodium molybdate, 500  $\mu$ M sodium fluoride, 100  $\mu$ M sodium orthovanadate, 1 mM EDTA, 40  $\mu$ g/ml PMSF, 10  $\mu$ g/ml aprotinin, 10  $\mu$ g/ml leupeptin, 0.7  $\mu$ g/ml pepstatin, 1 mM DIFP, 1 mM TLCK). Cytokine-stimulated cells were pelleted and lysed at 2 x 10<sup>7</sup> cells/ml as described (Welham and Schrader, 1992) with the exception that lysates were clarified for 5 min in a microfuge ay 4°C prior to further analyses. Immunoprecipitations were carried out as described (Welham *et al.*, 1994a) PDGF-receptor peptide (YpVPMLG) was coupled to Actigel according to the manufacturer's instructions. C-terminal antiserum to p110 $\delta$  was used for both immunoprecipitations and



immunoblotting. For p110 $\alpha$ , the C- and N-terminal antisera were used for immunoprecipitations and Westerns blot analysis, respectively.

SDS-PAGE and immunoblotting were carried out as described (Laemmli, 1970; Welham and Schrader, 1992; Welham *et al.*, 1994a). Antibodies were  
5 used at the following concentrations for immunoblotting: 4G10, antiphosphotyrosine monoclonal antibody at 0.1  $\mu$ g/ml; anti-p110 $\alpha$  and p110 $\delta$  at 0.25  $\mu$ g/ml; anti-p85 at 1:4000; anti-c-kit (Santa Cruz Biotechnology, sc-168) at 0.4  $\mu$ g/ml, anti-SHP (Santa Cruz Biotechnology, sc-280) at 0.1  $\mu$ g/ml and anti-IRS-2 (gift of Dr. M. White, Joslin Diabetes  
10 Center, Boston, MA) at 1:1000.

Both goat and anti-mouse and goat anti-rabbit horseradish peroxidase-conjugated antibodies (Dako, Denmark) were used at a concentration of 0.05  $\mu$ g/ml. Immunoblots were developed using the ECL system (Amersham). Blots were stripped and reprobed as previously described (Welham *et al.*,  
15 1994a).

### **Injection of CSF-1 Stimulated Mouse Macrophages with Antibodies to p110 $\delta$ and p110 $\alpha$**

The murine macrophage cell-line, BAC1, was used in antibody micro injection experiments. The peptide polyclonal antibodies to p110 $\delta$  were  
20 directed to either the C-terminal peptide 1044, (described p17 Materials and Methods), or to the peptide sequence (C)R222KKATVFRQPLVEQPED<sub>238</sub>. Polyclonal sera were affinity purified before micro injection and were used at a concentration of 0.5-5 mg/ml. A control peptide polyclonal antisera to human P110 $\alpha$  is as described on p17 of Materials and Methods. Before

micro injection, Bac1 cells were starved of Colony Stimulating Factor 1 (CSF1) for 24 hours. Antibodies were then injected into CSF1 starved cells and exposed to CSF1 for 10-15 minutes before visualisation of the cytoskeleton of micro injected Bac1 cells with phalloidin conjugated rhodamine, (preparation and visualisation of cells is as described in Allen et al 1997).

### Cell stimulations

Stimulation of cells with different growth factors was carried out as described (Welham and Schrader, 1992) with the exception that cells were resuspended at  $2 \times 10^7$ /ml in serum-free RPMI prior to stimulations. Chemically synthesized murine IL3 and IL4 were kindly provided by Dr. Ian Clark-Lewis (University of British Columbia, Vancouver). Recombinant murine SCF was purchased from R&D Systems Europe (Abingdon, Oxon). The concentration of growth factors and duration of stimulation (2 minutes for SCF; 10 minutes for IL3 and IL4) had been previously optimised to obtain maximal levels of tyrosine phosphorylation of receptors and cellular substrates. These were as follows, IL3 at 10  $\mu$ g/ml (Welham and Schrader, 1992), IL4 at 10  $\mu$ g/ml (Welham et al., 1994a) and SCF 50 ng/ml (M.J.W., unpublished observations).

### Northern blot analysis

Northern blots of human polyA<sup>+</sup> RNA (Clontech) were hybridized with random prime-labelled EcoRI fragment II of pBluescript clone 0<sub>9.1</sub>. Stripping and reprobing using the following subsequent probes was then performed: internal EcoRI-XhoI 2.1 kb fragment from human p110 $\alpha$  (Volinia et al.,

1994) and EcoRI-XhoI 5 kb cDNA of human p110 $\beta$  (C. Panaretou; unpublished results).

Using the above described materials and methods we were able to elucidate data which describes the novel lipid kinase and in particular a PI3 Kinase which we have termed p110 $\delta$ . Data relating to this kinase will now be described with a view to comparing p110 $\delta$  with other members of the PI3 Kinase group so as to compare and contrast their respective characteristics.

## RESULTS

### Cloning of p110 $\delta$

Degenerate primers based on conserved amino acid sequences (GDDLQRQD and FHI/ADFG) in the kinase domain of bovine p110 $\alpha$  and *S. cerevisiae* Vps34p were used in RT-PCR reactions with mRNA from the human MOLT4 T cell leukaemia. A partial cDNA, homologous but different from other known human PI3K, was obtained. This PCR fragment was used as a probe to screen a U937 monocyte library, and to isolate the corresponding full length clone (for details, see Materials and Methods and Fig. 9). Sequence analysis revealed a potential open reading frame, preceded by an in-frame stop codon. The potential start codon was also found to lie in a favourable context for translation initiation (Kozak, 1991). This open reading frame of 3135 nucleotides predicts a protein of 1044 amino acids with a calculated molecular mass of 119,471 daltons (Fig. 1A). Comparison of the amino acid sequence with other PI3K showed that this protein is most

5 closely related to human p110 $\beta$  (58% overall identity; Hu *et al.*, 1993), and more distantly to human p110 $\alpha$  (41% identity; Volinia *et al.*, 1994), human G-protein regulated p110 $\gamma$  (35% identity; Stoyanov *et al.*, 1995) and the human vps34p analogue (28% identity; Volinia *et al.*, 1995). The new PI3K described here will be further indicated as p110 $\delta$ .

10 Dot plot comparison at high stringency (Fig. 1B) shows that p110 $\alpha$ ,  $\beta$  and  $\delta$  are very homologous in the p85-binding region (AA 20-140 of p110 $\alpha$ ; Dhand *et al.*, 1994) as well as in the C-terminal PI-kinase (PIK) domain (HR2) and catalytic core (AA 529-end of p110 $\alpha$ , Zvelebil *et al.*, 1996). An additional region of high sequence homology, spanning AA 370-470 of p110 $\delta$ , was found in between the p85 binding site and HR2. This region contains the so-called HR3 signature (WxxxLxxxIxIxDLPR/KxAxL) which is conserved in all p85-binding PI3Ks and in p110 $\gamma$ . The most N-terminal area of sequence difference between p110 $\alpha$  and p110 $\beta/\delta$  overlaps with the region defined in p110 $\alpha$  as being sufficient for Ras binding (AA 133-314 in p110 $\alpha$ ; Rodriguez-Viciana *et al.*, 1996). Two additional structural motifs were identified in p110 $\delta$ . The first is a proline-rich region (Figure 1B, C) for which molecular modelling indicates that it can form a left-handed, polyproline type-II helix with the potential to interact with SH3 domains (data not shown). In the corresponding region, p110 $\alpha$  and p110 $\beta$  lack crucial prolines to allow a similar fold. The second motif is a basic-region, leucine-zipper (bZIP)-like domain, immediately C-terminal of HR3 (Figure 1B, C). A bZIP region is present in both p110 $\delta$  and p110 $\beta$  (and also in the *Drosophila* p110 (Leevers *et al.*, 1997)), whereas the basic component of this domain is less prominent in p110 $\alpha$  (Figure 1C). Modelling of the p110 $\delta$  ZIP region shows that its arrangement of L/V/I residues easily accommodates the formation of a helix structure which can form a coiled-coil dimeric protein

zipper complex (data not shown).

### **p110 $\delta$ binds the p85 adaptor and Ras proteins**

In order to verify the prediction from amino acid sequence comparison that p110 $\delta$  might bind p85 subunits, p110 $\delta$  was expressed in insect cells as a glutathione-S-transferase (GST)-fusion protein, together with recombinant baculoviruses encoding p85 $\alpha$ , p85 $\beta$  or p85 $\gamma$  (the latter is a 55 kDa bovine p85 isoform homologous to p55<sup>PIK</sup>, p55 $\alpha$  and p85/AS53 (Pons *et al.*, 1995; Inukai *et al.*, 1996; Antonetti *et al.*, 1996)). As is clear from Figure 2A all p85 adaptor subtypes efficiently co-purified with GST-p110 $\delta$  from co-infected cells.

The question of whether different class I p110 catalytic subunits show binding preference for different p85 adaptor proteins *in vivo* has not been previously addressed. Using antiserum specific for p110 $\delta$ , we found that both p85 $\alpha$  and p85 $\beta$  were present in p110 $\delta$  immunoprecipitates from different white blood cells (Figure 2B shows the data for human neutrophils; note that p85 $\gamma$  is not expressed in leukocytes). Similar results were obtained for p110 $\alpha$  (data not shown). In these immune complexes, a 45 kDa protein reactive with p85 $\alpha$  antibodies was also observed (Figure 2B). The nature of this protein is currently unclear, but it might be similar to a 45 kDa protein previously described to be present in p85 and p110 IPs from various tissues (Pons *et al.*, 1995).

P110 $\alpha$  and p110 $\beta$  have been shown to interact with Ras-GTP (Kodaki *et al.*, 1995; Rodriguez-Viciano *et al.*, 1994 and 1996). The region required for this interaction lies between AA 133 and 314 of these PI3Ks (Rodriguez-Viciano

*et al.*, 1996). Despite the relatively low sequence conservation with p110 $\alpha$  and p110 $\beta$  in this region (Figure 1C), certain apparently critical amino acids are conserved as p110 $\delta$  does interact with Ras *in vitro*, in a GTP-dependent manner (Figure 2C).

## 5     **p110 $\delta$ binds ras, but not rac or rho**

Incubation of GST-p110 $\delta$ /p85 $\alpha$  was found to retain GTP-bound wild-type ras or oncogenic V12-ras (**Fig. 2C**). This was not the case with GDP-loaded ras, or with A38-ras, a functionally dead ras mutant. Similar as for p110 $\alpha$ , no binding of rho and rac could be demonstrated (**data not shown**).

## 10    **Lipid kinase activity of p110 $\delta$**

When tested in the presence of Mg<sup>2+</sup>, p110 $\delta$  was found to phosphorylate PtdIns, PtdIns4P and PtdIns(4,5)P<sub>2</sub> (**Fig. 3A**). HPLC analysis confirmed that these lipids are phosphorylated at the D3 position (**Fig. 3B**). Substrate preference *in vitro* was PtdIns > PtdIns4P > PtdIns(4,5)P<sub>2</sub> (**data not shown**).

15    Lipid kinase activity was lower in the presence of Mn<sup>2+</sup> than in the presence of Mg<sup>2+</sup> (tested over the concentration range of 0.25 to 16 mM; **data not shown**). Specific activity of p110 $\delta$ , isolated from Sf9 cells, was a factor 2-5 lower than that of p110 $\alpha$  (**data not shown**). Taken together, these data establish p110 $\delta$  as a genuine class I PI3K.

## 20    **P110 $\delta$ does not phosphorylate p85 but autophosphorylates.**

The p85 subunit has been demonstrated to be a substrate for a Mn<sup>2+</sup>-dependent phosphorylation by the p110 $\alpha$  catalytic subunit (Carpenter *et al.*,

1993; Dhand *et al.*, 1994). In contrast, GST-p110 $\delta$  failed to phosphorylate coexpressed p85 $\alpha$ , p85 $\beta$  or p85 $\gamma$  under a variety of *in vitro* conditions (partial data shown in Fig. 4A; no activity was seen either in the presence of Mg<sup>2+</sup> or Mn<sup>2+</sup>). p85 $\gamma$  lacks an SH3 domain, and the absence of phosphorylation of this molecule by p110 $\delta$  argues against the possibility that an intermolecular interaction of the p85 $\alpha/\beta$  SH3 domain with the p110 $\delta$  proline-rich region is locking up the p85 molecules for efficient phosphorylation by p110 $\delta$ . In order to exclude that p110 $\delta$  had already fully phosphorylated p85 during the *in vivo* co-expression in insect cells, exogenous purified p85 $\alpha$  was added to immobilized GST-p110 $\delta$ . After washing away the excess p85, bound p85 was found to be efficiently phosphorylated by p110 $\alpha$ , but again not by p110 $\delta$  (data not shown). When untagged p110 $\delta$ , in complex with p85 $\alpha$  or p85 $\beta$ , was subjected to an *in vitro* kinase assay in the presence of Mn<sup>2+</sup>, p110 $\delta$  autophosphorylated ((Fig. 4B note that this activity is largely absent in immobilised GST-p110 $\delta$  (Fig. 4B)). Such phosphorylation was not seen in p110 $\alpha$ /p85 complexes, in which again p85 was found to be phosphorylated (Fig. 4B). Phosphoamino acid analysis showed that the phosphorylation on p110 $\delta$  occurred on serine (Fig. 4B). Both the phosphorylation of p85 by p110 $\alpha$  and the autophosphorylation of p110 $\delta$  were observed to be largely Mn<sup>2+</sup>- dependent, with only very weak phosphorylation in the presence of Mg<sup>2+</sup> (data not shown). Autophosphorylation of p110 $\delta$  resulted in reduced lipid kinase activity.

In order to exclude the possibility that the observed phosphorylation of p110 $\delta$  was due to a coprecipitated protein kinase, a kinase-defective p110 $\delta$  mutant was generated. This was done by converting arginine 894 to proline in p110 $\delta$ , generating p110 $\delta$ -R894P. The mutated arginine residue is located in the conserved DRX<sub>3</sub>NX<sub>12-13</sub>DFG motif of the kinase domain, likely to be part

of the catalytic loop as in protein kinases (Taylor *et al.*, 1992, Zvelebil *et al.*, 1996). A similar mutation in bovine p110 $\alpha$  (R916P) has been found to completely knock out catalytic activity (Dhand *et al.*, 1994). As is clear from **Fig. 4C**, p110 $\delta$ -R894P, expressed in insect cells, was no longer phosphorylated in precipitates of p110 $\delta$ , indicating that the latter has indeed autophosphorylation capacity. Likewise, lipid kinase activity was found to be lost by p110 $\delta$ -R894P (data not shown).

We have produced polyclonal antisera to the phosphorylated form of p110 $\delta$ . The C-terminal peptide sequence 1044 was phosphorylated at the serine residue 1033 and used to immunize rabbits. The antisera directed against the phosphorylated peptide has enabled us to establish that p110 $\delta$  is phosphorylated *in vivo* and upon cytokine stimulation this phosphorylation is enhanced (results not shown).

#### Drug sensitivity of p110 $\delta$ catalytic activity

p110 $\alpha$  and  $\delta$  lipid kinase activity were found to exhibit a similar sensitivity to inhibition by wortmannin and LY294002 (**Fig.5**), with an IC<sub>50</sub> of 5 nM (for wortmannin) and 0.5  $\mu$ M (for LY294002). Likewise, the autophosphorylation activity of p110 $\delta$  was also inhibited by wortmannin in the nanomolar range (data not shown)

#### Tissue distribution of p110 $\delta$

The expression pattern of p110 $\delta$  was investigated by Northern blot analysis of polyA<sup>+</sup> RNA of human tissues, and compared with that of p110 $\alpha$  and p110 $\beta$ . A single messenger mRNA species of approximately 6 kb was found



to be particularly highly expressed in white blood cell populations i.e. spleen, thymus and especially peripheral blood leucocytes (the latter contains all white blood cells with only the majority of the erythrocytes being removed) (**Fig. 6**). In some Northern blot experiments, an additional ~5 kb messenger  
5 for p110 $\delta$  was also observed (data not shown). Low levels of p110 $\delta$  messenger RNA expression were found in most other tissues examined, although it is difficult to exclude the possibility that blood cell contamination is responsible for this p110 $\delta$  mRNA signal. p110 $\alpha$  and p110 $\beta$  were also found to be expressed in most tissues examined (**Fig. 6**).

10 Antibodies specific for p110 $\alpha$  and  $\delta$  were then used to assay the expression of these PI3K at the protein level. Upon testing different rat tissues, a 110 kDa protein reactive with p110 $\delta$  antibodies was found in spleen and thymus, but not in any of the other tissues tested (**Fig. 7**). This pattern largely confirms the data of the Northern blot analysis described above. p110 $\delta$  was  
15 also found to be present in both primary and transformed white blood cells, independent of their differentiation stage (**Fig. 7**). In the primary blood cells, both the lymphoid and myeloid cell populations were positive for p110 $\delta$  whereas platelets were not (**Fig. 7**). Both T (e.g. Jurkat, HPB All) and B (e.g. Raji, HFB1) cell lines expressed p110 $\delta$  (**Fig. 7**). The 110 kDa  
20 p110 $\delta$  was not found in Rat-1, NIH 3T3 and Swiss 3T3 fibroblasts, LS174T and COLO 320HSR colon adenocarcinomas, A431 epidermoid carcinoma, ECC-1 endometrial carcinoma and HEp-2 larynx carcinoma (**Fig. 7**) nor in CHO chinese hamster ovary, POC small-cell lung cancer cell line, porcine and bovine aortic endothelial cells, MDA-MB-468 breast adenocarcinoma,  
25 and primary human muscle and fibroblasts (data not shown). In conclusion, it appears that p110 $\delta$  is selectively expressed in leukocytes.

In contrast to p110 $\delta$ , p110 $\alpha$  was found in most of the tissues and cell lines investigated, including the white blood cells (Fig. 7).

### **Micro Injection of Anti p110 $\delta$ Polyclonal Antibodies Into CSF-1 Stimulated Murine Macrophages**

5 The possible function of p110 $\delta$  was investigated further by a series of micro injection experiments of the murine macrophage cell-line, Bac1 with antisera to p110 $\delta$  and p110 $\alpha$ . Prior to micro injection, Bac1 cells were deprived of CSF1 for 24 hours. CSF1 deprivation primes cells to divide and become motile when subsequently exposed to CSF1. Affinity purified anti p110 $\delta$   
10 polyclonal antibodies were micro injected into CSF1 deprived Bac1 cells followed by exposure to CSF1 for 10-15 minutes.

The micro injected Bac1 cells show marked alterations in cellular morphology. The normal cell membrane ruffling disappears and cytoplasmic retraction occurs. The cytoskeleton of micro injected Bac1 cells was  
15 visualised using a phalloidin-rhodamine conjugate and figure 10 shows a representative sample of such cells showing a disorganised cytoskeletal arrangement. The injection of anti p110 $\alpha$  does not produce an equivalent effect.

Interestingly a similar phenotype is shown by expression of the dominant-  
20 negative small GTP-binding protein rac, N17RAC. This suggests that p110 $\delta$  may be part of the same signalling cascade that may be involved in cytoskeletal organisation and cellular motility.

**p110 $\delta$  is involved in cytokine signalling**

In leucocytes, p85-binding PI3Ks have been implicated in a wide variety of signalling events including signalling via cytokine and complement receptors, integrins, Fc receptors, B and T cell antigen receptors and their accessory molecules such as CD28 (reviewed by Stephens et al., 1993; Fry, 1994).

5 Therefore, it is clear that a multitude of signalling processes could be potentially linked to p110 $\delta$ . A crucial question is whether selective coupling of p110 $\delta$  to the above-mentioned signalling/receptor complexes occurs in cells that also contain other class I PI3K, given the observation that different p110s seem to be complexed with the same p85 isoforms (**Fig. 2B**). We  
10 addressed this important question in the context of cytokine signal transduction, operative in diverse types of leukocytes.

Different families of cytokines transduce signals via discrete classes of receptors that share common gp130,  $\beta$  or  $\gamma$  chains, or via receptors with intrinsic tyrosine kinase activity (reviewed in Taga and Kishimoto, 1995):

15 Whereas PI3K activation by cytokines signalling via gp130 has not been reported, activation of p85-binding PI3K in response to cytokine signalling via the common  $\beta$  chain (eg IL3), common  $\gamma$  chain (eg IL4), or via tyrosine kinase receptors (such as c-kit, which binds Stem Cell Factor (SCF)) has been demonstrated (Wang et al, 1992; Gold et al, 1994). We examined the ability  
20 of IL3, IL4 and SCF to couple to p110 $\delta$  and p110 $\alpha$  in cytokine-dependent leukocyte cell lines. An identical pattern of phosphotyrosine-containing proteins, specific to the cytokine used for stimulation, was found to co-precipitate with p110 $\alpha$  and p110 $\delta$  antibodies (**Fig. 8, panel a**). In the IL3- and IL4- responsive Ba/F3 pre-B and myeloid progenitor FD-6 cell lines (**Fig. 8A; data for FD-6 are not shown**), IL3-treatment induced the appearance  
25 in p110 $\alpha$ / $\delta$  IPs of an unknown protein of 100 kDa and the 70 kDa protein tyrosine phosphatase, SHP2 (**Fig. 8A, panel b**). The 170 kDa protein co-

precipitated upon IL4 stimulation (Fig. 8A, panel a) was shown by immunoblotting to be IRS-2, the major substrate of IL4-induced phosphorylation in these cells (data not shown). Fig. 8B shows the results of similar analyses in MC/9 mast cells. Following SCF stimulation, both p110 $\alpha$  and p110 $\delta$  IPs contained an unidentified 100 kDa tyrosine-phosphorylated protein as well as a 150 kDa protein identified as c-kit, the SCF receptor (Fig. 8B, panels a and b). Taken together, these data indicate that p110 $\alpha$  and p110 $\delta$  show no apparent differences in their recruitment to a variety of activated cytokine receptor complexes. In addition, the implication in cytokine signalling of at least two members of the p85-binding PI3K class reveals a previously unrecognised complication of signal transduction pathways downstream of these cytokine receptors.

#### **Expression of PI3 Kinase p110 Sub Units in Murine and Human Melanoma Cell-Lines.**

The expression of p110 $\delta$  was further investigated in various murine and human melanoma cell-lines. A characteristic feature of a melanoma is the aggressive nature of the metastasis associated with this cancer. The possible involvement of p110 $\delta$  in metastasis was investigated by analysing the relative abundance of p110 $\delta$  protein in a range of murine and human cell-lines. Western blots were used to assess the levels of p110 $\alpha$  and  $\beta$  as well as p110 $\delta$ . J774, a murine cell-line, was used as a positive control for the murine western blots. Neonatal melanocytes were used as a control for the human western blot. Table 1 indicates that p110 $\alpha$  and  $\beta$  are constitutively expressed in both control and melanoma cell-lines of both murine and human origin. Interestingly, the murine control cell-line J744 shows markedly reduced levels of p110 $\delta$  when compared to the murine melanoma cell-lines.

However detectable levels of p110 $\delta$  are found in human neonatal melanocytes. This may be explained by the nature of these human control cells. The expression of p110 $\delta$  in these control cells may be explained by the relatively recent migration of these cells in the human skin and therefore residual levels of p110 $\delta$  may be present in these cells. Adult melanocytes have prolonged residence in skin and the level of p110 $\delta$  may be reduced to undetectable levels commensurate with their terminal differentiation.

We have described a novel human p110 subunit, p110 $\delta$ , which is part of the PI3 kinase family. p110 $\delta$  shows a restricted expression pattern, only accumulating to significant levels in white blood cells populations and particularly in peripheral blood leucocytes. The motile nature of these cells has lead us to propose that this member of the PI3 kinase family may be involved in regulating the motility of cells via cytoskeletal reorganisation. The data relating to murine and human melanoma cell lines is interesting but inconclusive with regard to human melanomas. The use of tissue biopsies of normal human melanocytes and human melanomas will allow this to be resolved.

Table 1.

## Expression of p110 Subunits in Murine Melanomas

Cell-line	Characteristic	$\delta$	$\alpha$	$\beta$	Reference
<u>Murine</u>					
J774	Control	-	+	+	This study
Melan-c	Melanoma	-	+	+	
Melan-pl	Melanoma	-	+	+	Wilson et al 1989
Melan-a	Melanoma	-	+	+	Wilson et al 1989
Tu-2d					
Mel-ab	Melanoma	+/-	+	+	Dooley et al 1988
Mel-ab-LTR-Ras2	Melanoma	+	+	+	Dooley et al 1988
Mel-ab-LTR Ras 3	Melanoma	+	+	+	Dooley et al 1988
Mel-ab-pMT	Melanoma	+	+	+	Dooley et al 1988
B16 F1	Melanoma (weakly metastatic)	+	+	+	Fidler et al 1975
B16 F10	Melanoma (highly metastatic)	+	+	+	Fidler et al 1975

Table 1 Continued

## Expression of p110 Subunits in Human Melanomas

Cell-line	Characteristic	$\delta$	$\alpha$	$\beta$	Reference
<u>Human</u>					
A375P	Melanoma (weakly metastatic)	-	+	+	Easty et al 1995
A375M	Melanoma (highly metastatic)	+	+	+	Easty et al 1995
WM164	Melanoma	+	+	+	Easty et al 1995
WM451	Melanoma	+	+	+	Easty et al 1995
DX3	Melanoma (weakly metastatic)	+	+	+	Ormerod et al 1986
DX3-LT5.1	Melanoma (Highly metastatic)	-	+	+	Ormerod et al 1986
Control (human neonatal melanocytes)	Primary cells	+	+	+	This study

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### CLAIMS

1. An isolated autophosphorylating polypeptide, or fragment thereof, possessing PI3 kinase activity represented by the amino acid sequence shown  
5 in Figure 1, or a homologue or analogue thereof, optionally modified by deletion, substitution or addition of at least one amino acid residue and showing selective expression in white blood cells and/or melanomas.
2. An isolated polypeptide according to Claim 1 wherein said polypeptide is capable of association with at least one mammalian p85 adaptor  
10 polypeptide.
3. An isolated polypeptide according to Claims 1 and 2 wherein said polypeptide is characterised by a domain having a proline content between 35-45%.
4. An isolated polypeptide according to Claim 3 wherein said proline rich  
15 domain is ideally at position 292-311 of the protein sequence data shown in Figure 1 but may be at an homologous/analogous site in an equivalent PI3 kinase.
5. An isolated polypeptide according to Claims 1-4 wherein said polypeptide is of mammalian origin and ideally human.
- 20 6. An isolated nucleic acid molecule that encodes the polypeptide according to Claims 1-5.

7. An isolated nucleic acid molecule according to Claim 6 wherein the nucleic acid sequence is either cDNA or genomic DNA.
- 8 An isolate nucleic acid molecule according to Claims 6 and 7 wherein said molecule is in a cloned recombinant vector.
- 5 9. An isolated nucleic acid molecule according to Claims 6-8 wherein said molecule, or part thereof, is adapted for the recombinant expression of the polypeptide according to Claims 1-5.
- 10 10. A host cell, transfected or transformed using the construct of the invention according to Claim 8 or 9 wherein said construct directs the recombinant synthesis of a whole or a part of the polypeptide according to Claims 1-5.
- 11 A host cell line according to Claim 8 wherein said cell line is an insect cell line.
- 15 12. The use of the recombinantly expressed polypeptide according to Claims 8 and 9 or the isolated polypeptide according to Claims 1-5 for the production of antibodies to p110 $\delta$ .
13. An antibody, or part thereof, according to Claim 12 wherein said antibody is monoclonal.
- 20 14. A method for the identification of the tissue specific expression of the polypeptide according to Claims 1-5 comprising determining the presence of either, or both, the relevant polypeptide and/or the mRNA and/or cDNA

encoding same.

15. A method according to Claim 14 wherein said method comprises binding at last two nucleic acid molecule primers adapted to hybridise to at least one selected part of the nucleic acid molecule of the invention to the  
5 said cDNA.

16. A method according to Claim 14 or 15 wherein said method comprises providing the conditions for amplifying and purifying at least one part of said nucleic acid molecule according to Claims 6-11 using said primers.

17. A method according to Claim 14 wherein said method comprises using  
10 an antibody according to Claims 12 or 13 for the detection of said polypeptide wherein said use involving either ELISA, western blot, immunoprecipitation or immunofluorescence.

18. A method for identifying agents effective at modulating the kinase activity of the polypeptide, according to Claims 1-5 comprising exposing the  
15 polypeptide, either *in vitro* or *in vivo*, to agents that may have modulating effects and then observing the kinase activity of said polypeptide.

19. A method according to Claim 18 wherein potentially antagonistic agents are screened using computer aided modelling or conventional laboratory techniques.

20. A method according to Claims 18 or 19 wherein cells, expressing the polypeptide according to Claims 1-5, are exposed to potential antagonistics and the motility of said cells is monitored.

21. A pharmaceutical/veterinary composition comprising an agent effective at modulating the activity of the polypeptide of the invention.

22. A pharmaceutical/veterinary composition according to Claim 21 which optionally also includes a diluant, carrier or excipient and/or is in unit dosage form.

23. A method for controlling the motility of cells comprising exposing a population of cells to either the polypeptide according to Claims 1-4, or an antagonist or an agonist thereof.

24. A method according to Claim 23 wherein the motility of cells is enhanced by exposure of the cells to the polypeptide of the invention.

25. Use of an agent effective at blocking the activity of the polypeptide according to Claims 1-5 for controlling cell motility.

26. Use of the polypeptide according to Claims 1-5 for enhancing cell motility.

27. Antisense oligonucleotide adapted to hybridize to the nucleic acid of Claims 6-9.

28. Antisense oligonucleotide according to Claim 27 wherein said oligonucleotide is modified as hereindescribed.

29. A pharmaceutical/veterinary composition comprising the antisense oligonucleotide of Claim 27 or 28.

Figure 1

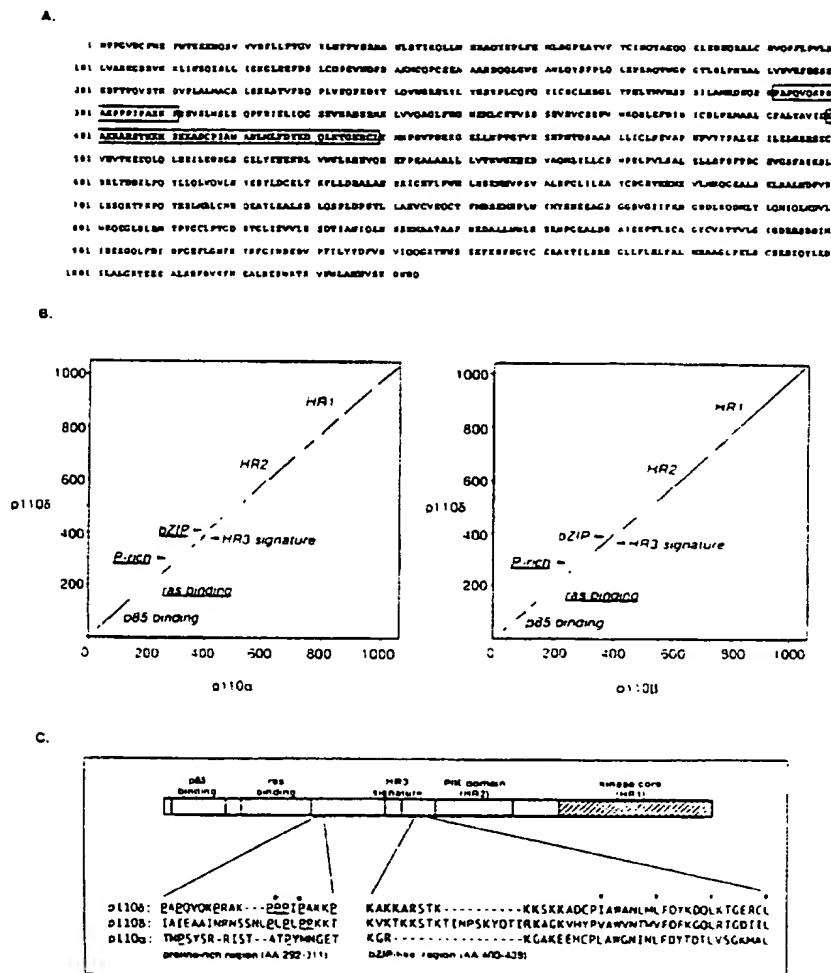


Figure 2A

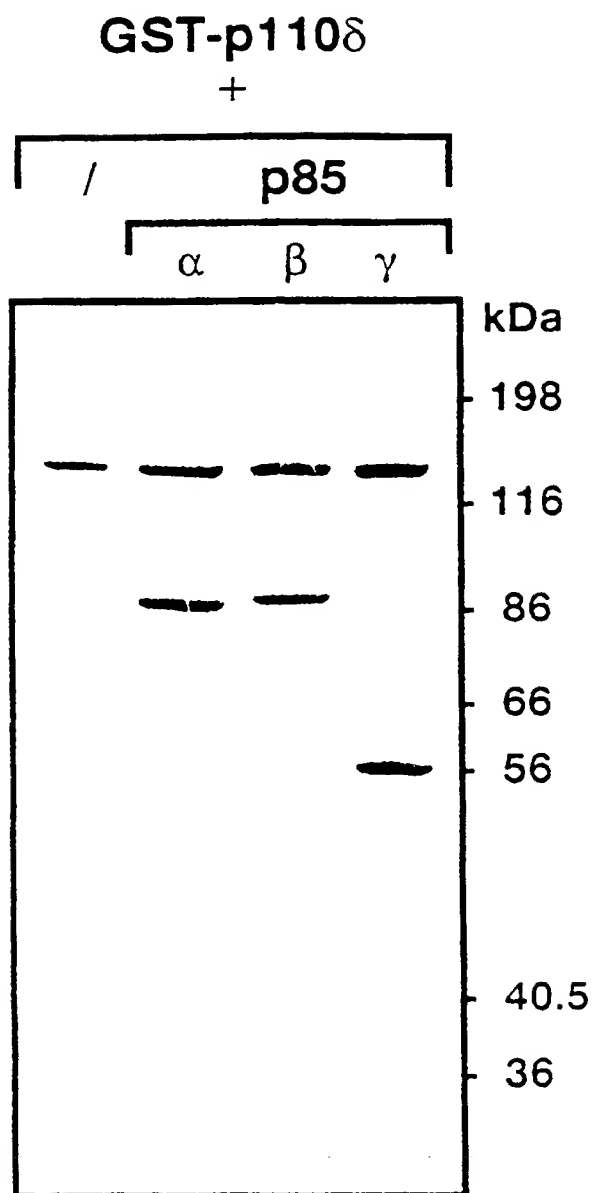


Figure 2B

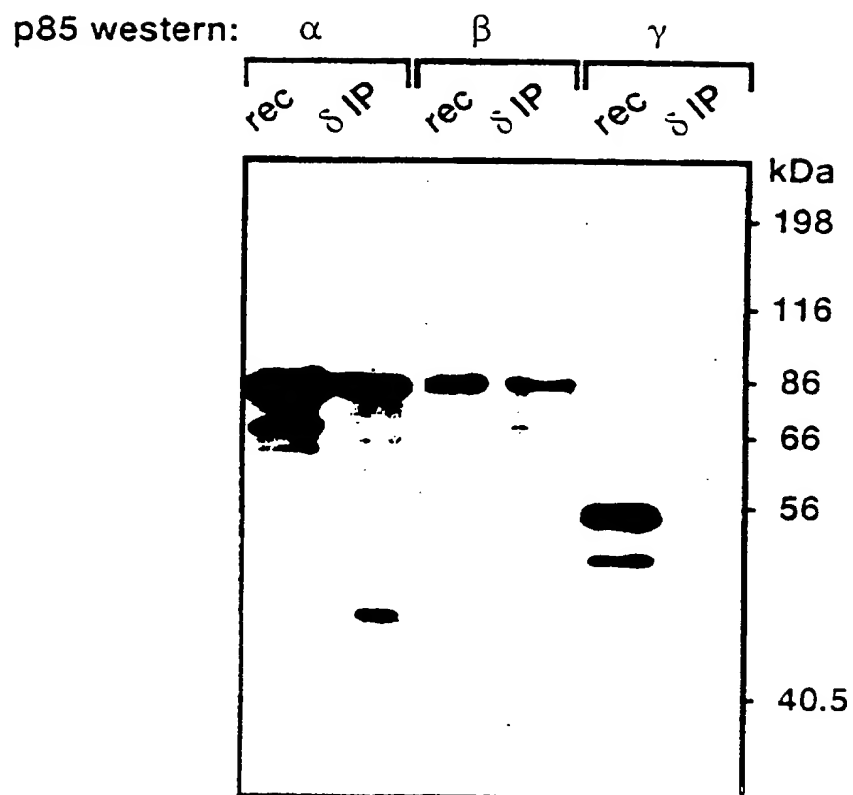


Figure 2C

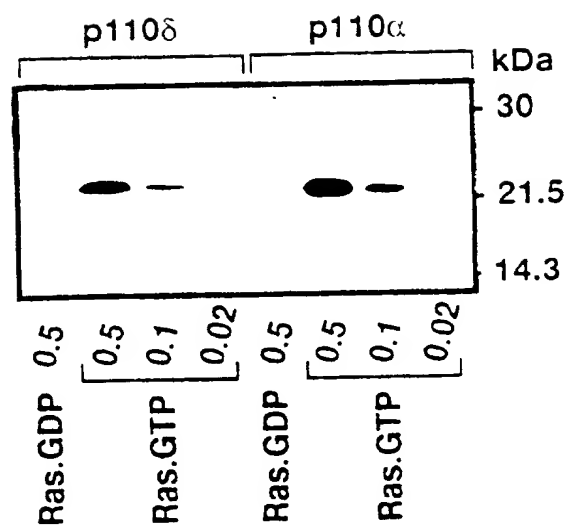




Figure 3A

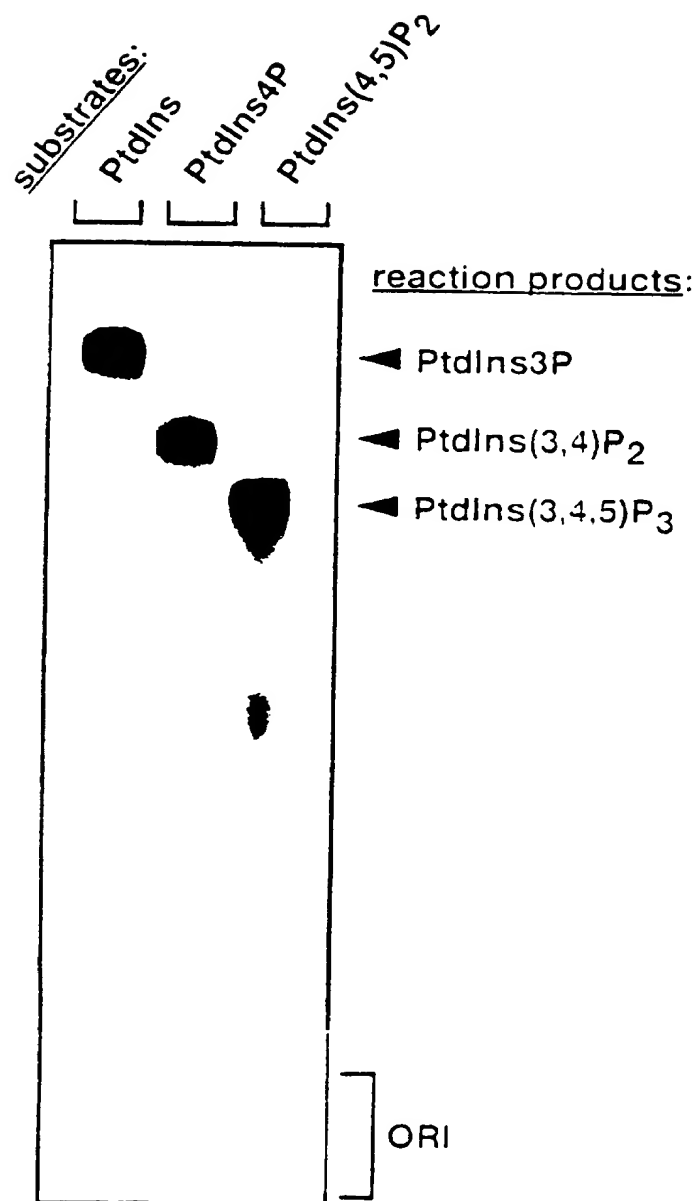


Figure 3B

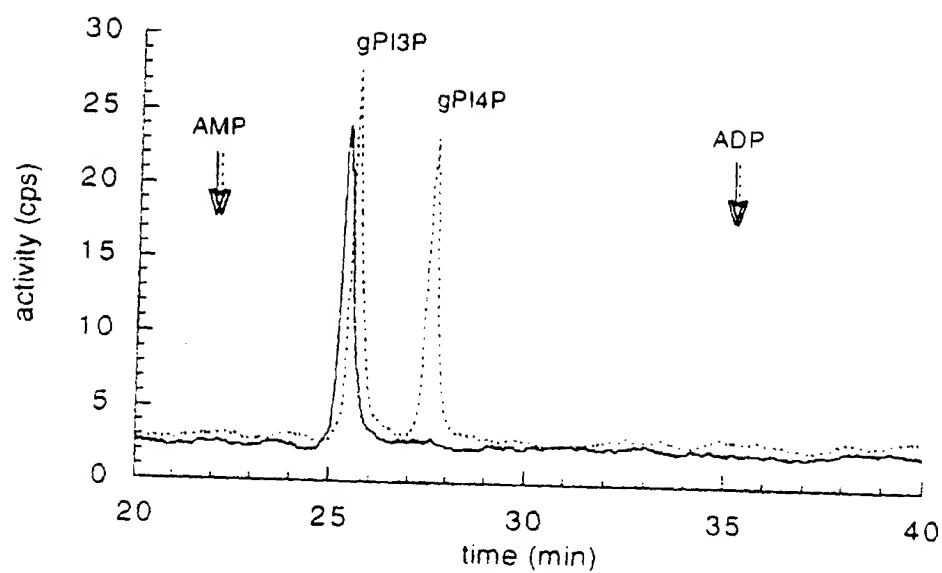


Figure 4A

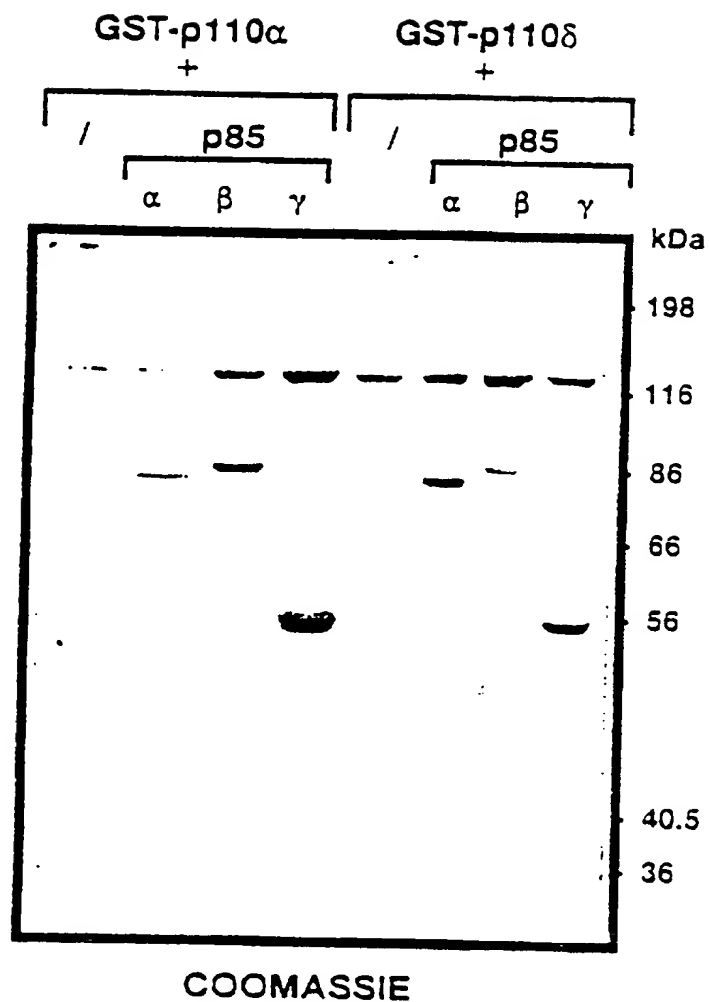


Figure 4A Cont/d

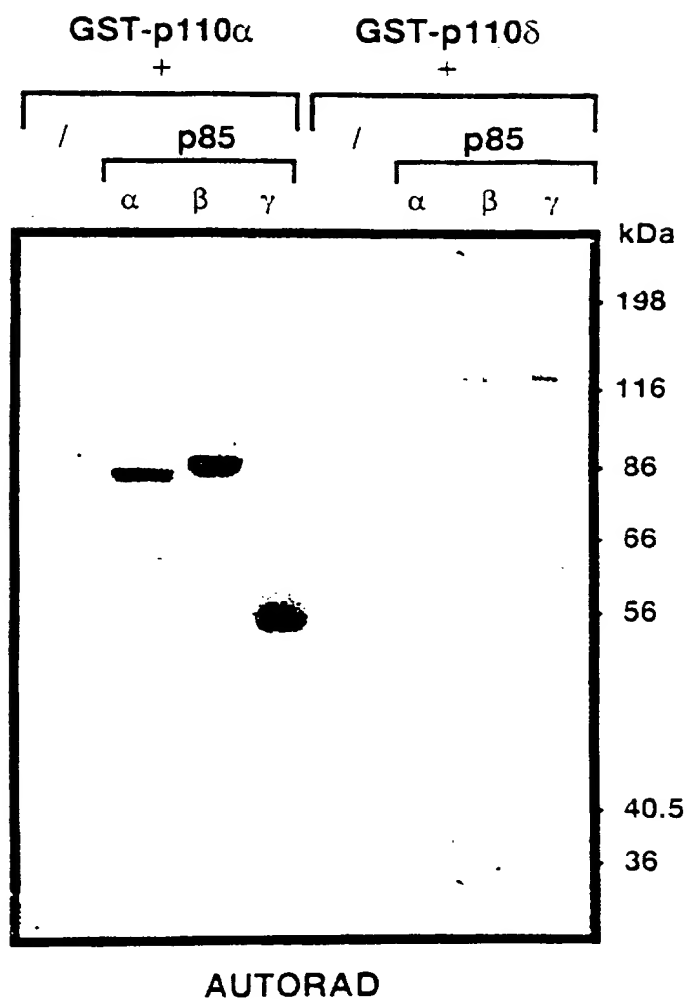


Figure 4B

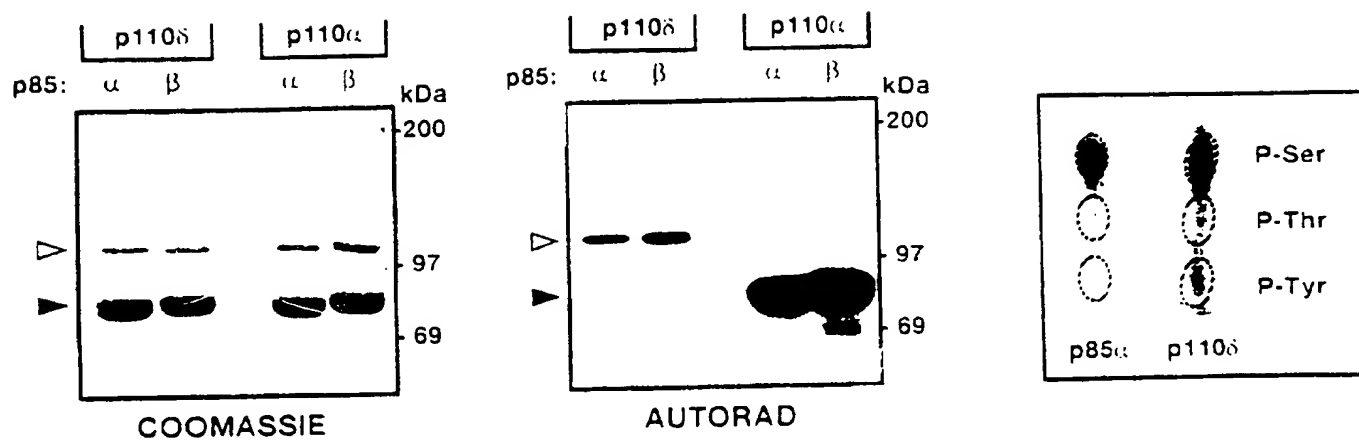


Figure 4C

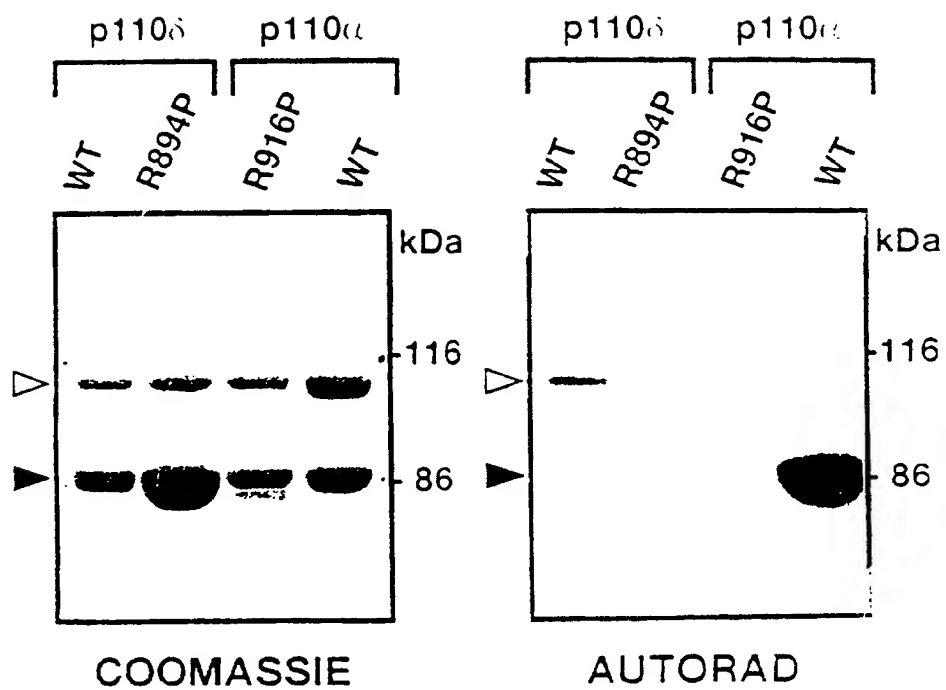


Figure 5

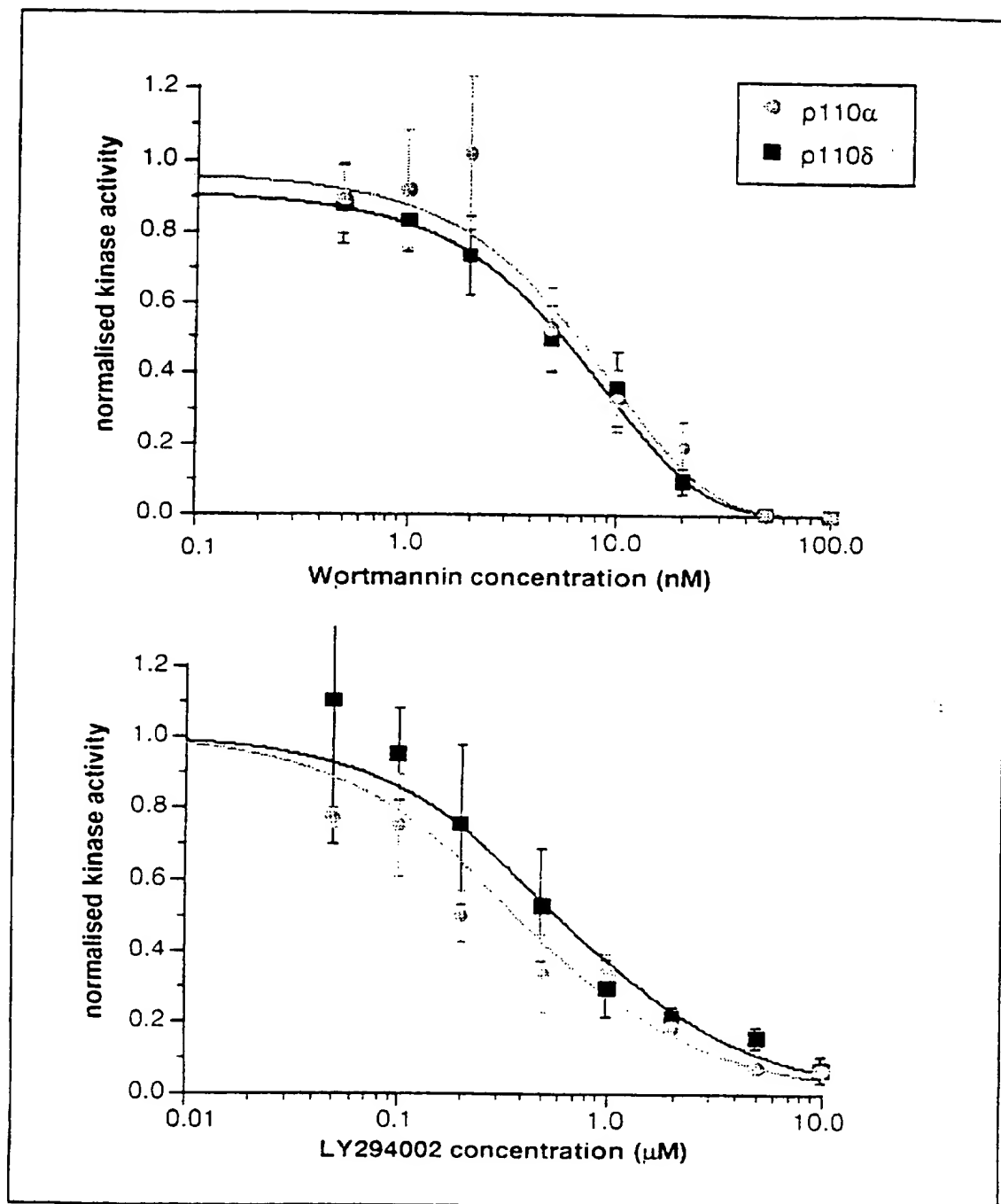


Figure 6

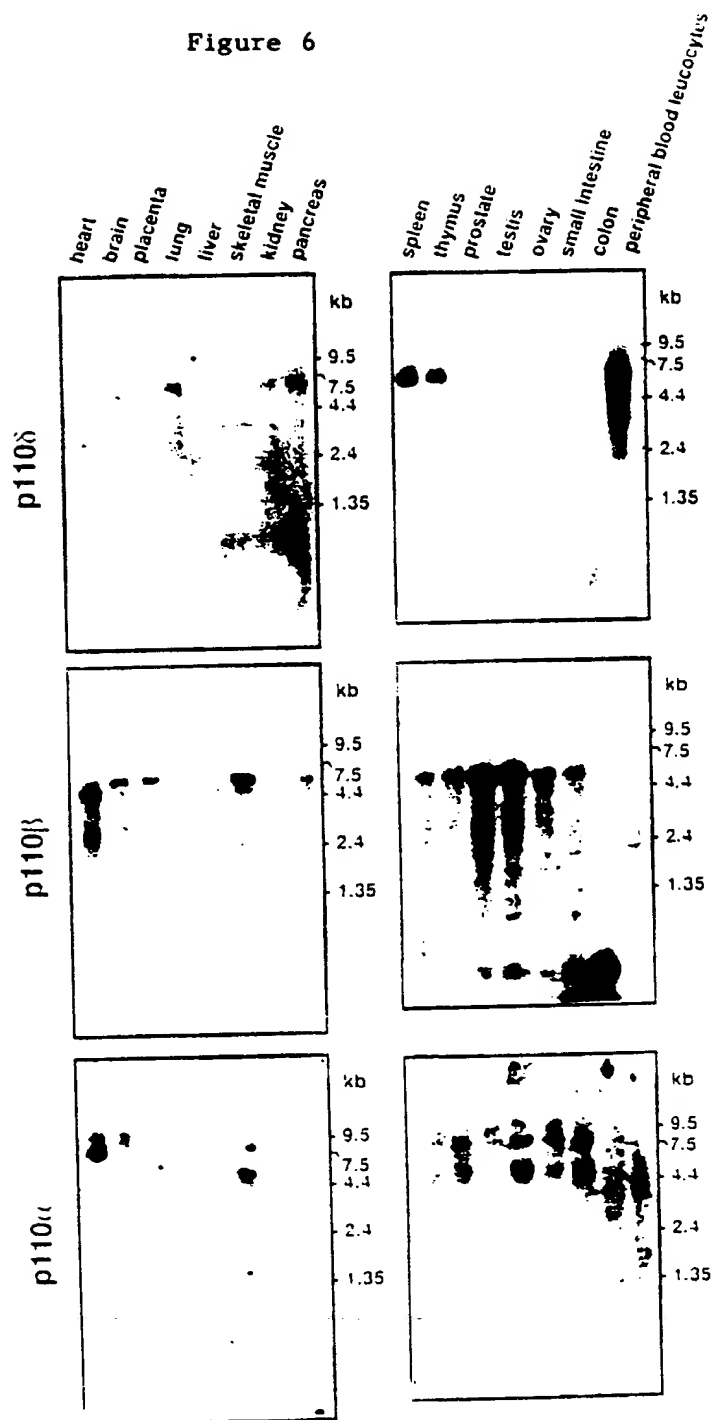




Figure 7

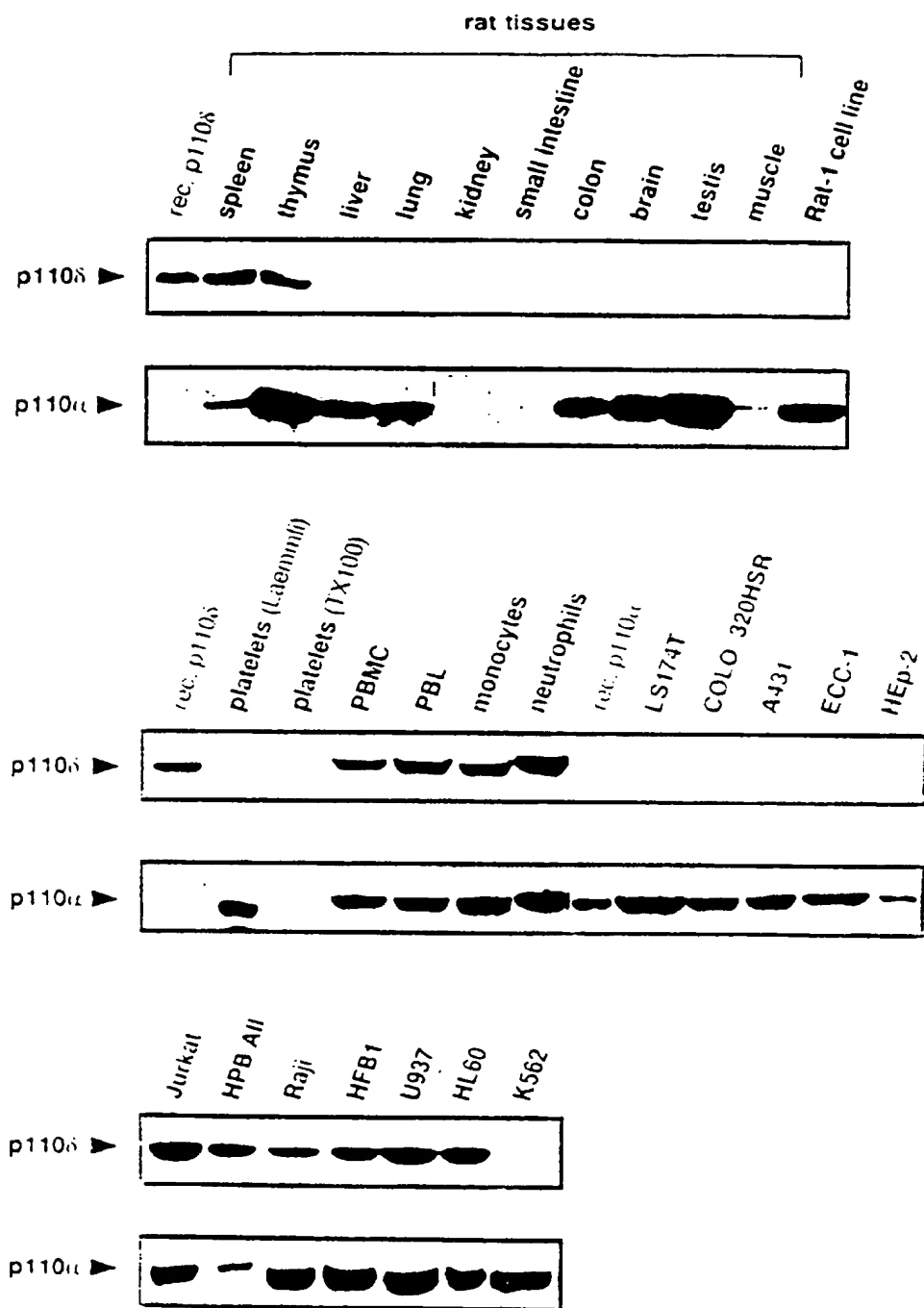


Figure 8

## A. Ba/F3

## B. MC/9

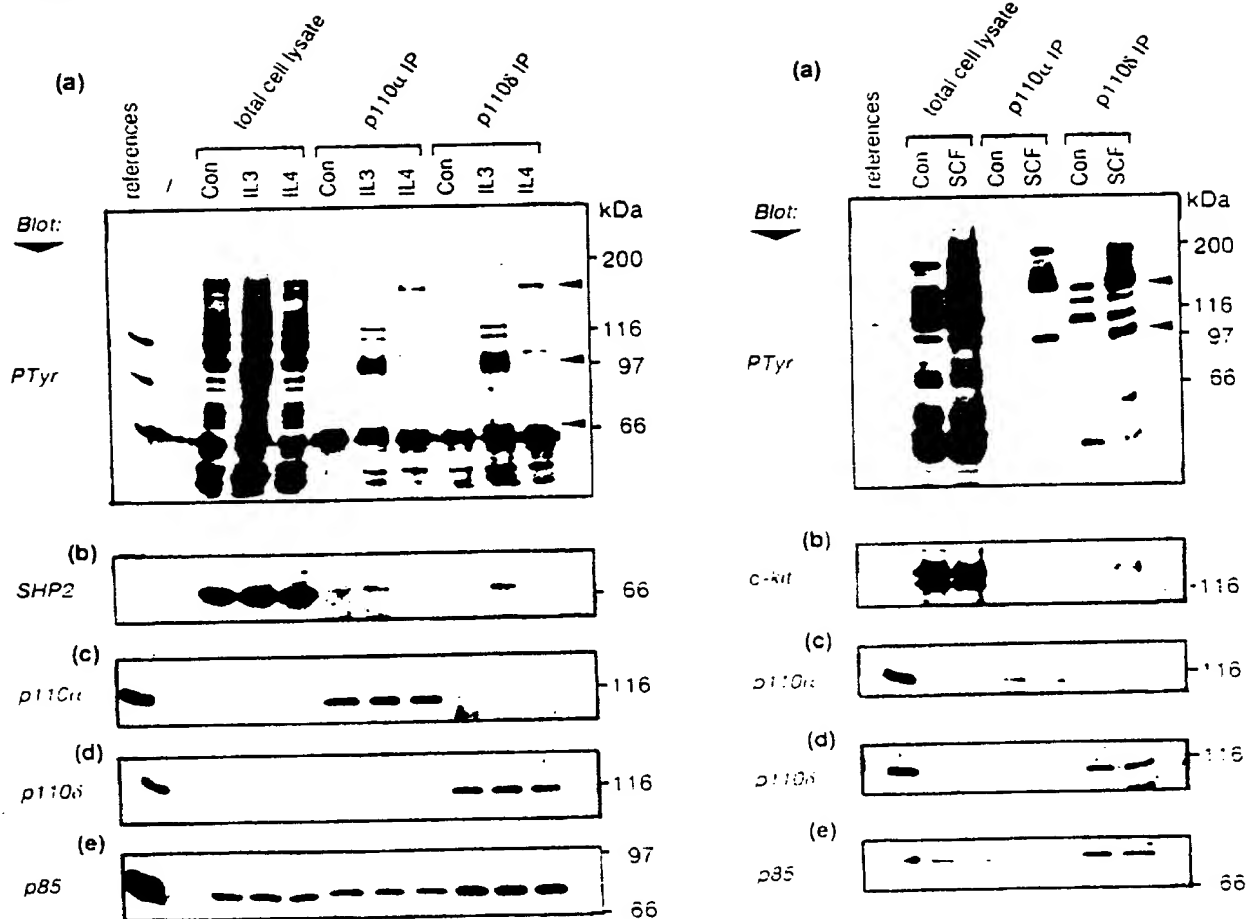


Figure 9

1 ATGCCCCCTG GGGTGGACTG CCCCATGGAA TTCTGGACCA AGGAGGAGAA  
 51 TCAGAGCGTT GTGGTTGACT TCCTGCTGCC CACAGGGGTC TACCTGAACT  
 101 TCCCTGTGTC CCGCAATGCC AACCTCAGCA CCATCAAGCA GCTGCTGTGG  
 151 CACCGCGCCC AGTATGAGCC GCTCTTCCAC ATGCTCAGTG GCCCCGAGGC  
 201 CTATGTGTTC ACCTGCATCA ACCAGACAGC GGAGCAGCAA GAGCTGGAGG  
 251 ACGAGCAACG GCGTCTGTGT GACGTGCAGC CCTTCCTGCC CGTCCTGCGC  
 301 CTGGTGGCCC GTGAGGGCGA CCGCGTGAAG AAGCTCATCA ACTCACAGAT  
 351 CAGCCTCCTC ATCGGCAAAG GCCTCCACGA GTTTGACTCC TTGTGCGACC  
 401 CAGAAGTGAA CGACTTTCGC GCCAAGATGT GCCAATTCTG CGAGGAGGCG  
 451 GCCGCCCCGC GGCAGCAGCT GGGCTGGGAG GCCTGGCTGC AGTACAGTTT  
 501 CCCCCTGCAG CTGGAGCCCT CGGCTCAAAC CTGGGGGGCT GGTACCCTGC  
 551 GGCTCCCGAA CCGGGCCCTT CTGGTCAACG TTAAGTTTGA GGGCAGCGAG  
 601 GAGAGCTTCA CCTTCCAGGT GTCCACCAAG GACSTGCCGC TGGCGCTGAT  
 651 GGCCTGTGCC CTGCGGAAGA AGGCCACAGT GTTCGGGCAG CCGCTGGTGG  
 701 AGCAGCCGGA AGACTACACG CTGCAGGTGA ACGGCAGGCA TGAGTACCTG  
 751 TATGGCAGCT ACCCGCTCTG CCAGTTCCAG TACATCTGCA GCTGCCTGCA  
 801 CAGTGGGTG ACCCCTCACC TGACCATGGT CCATTCCCTCC TCCATCCTCG  
 851 CCATGCGGGA TGAGCAGAGC AACCCCTGCC CCCAGGTCCA GAAACCGCGT  
 901 GCCAAACCAC CTCCCATTCC TGCGAAGAAG CCTTCCTCTG TGTCCCTGTG  
 951 GTCCCTGGAG CAGCCGTTCC GCATCGAGCT CATCCAGGGC AGCAAAGTGA  
 1001 ACSCCBACGA GCGGATGAAG CTGGTGGTGC AGGCTGGGCT TTTCCACGGC  
 1051 AACGAGATGC TGTGCAAGAC GGTGTCCAGC TGGAGGTGA GCSTGTGCTC  
 1101 GGAGCCCGTG TGAAGCAGC GGCTGGAGTT CGACATCAAC ATCTGCGACC  
 1151 TGCCCGCAT GGCCCGTCTC TGCTTTGCGC TGTACGCGT GATCGAGAAA  
 1201 GCCAAGAAGG CTCGCTCCAC CAAGAAGAAG TCCAAGAAGG CGGACTGCCC  
 1251 CATGGCTGG GCCAACCTCA TGCTGITTGA CTACAAGGAC CAGCTTAAGA  
 1301 CCGGGGAACG CTGCCTCTAC ATGTGGCCCT CCGTCCCAGA TGAGAAGGGC  
 1351 GAGCTGCTGA ACCCCACGGG CACTGTGCGC AGTAACCCCA ACACGGATAG  
 1401 CGCCGCTGCC CTGCTCATCT GCCTGCCCGA GGTGGCCCG CACCCCGTGT  
 1451 ACTACCCCGC CCTGGAGAAG ATCTGGAGC TGGGCGGACA CAGCGAGTGT

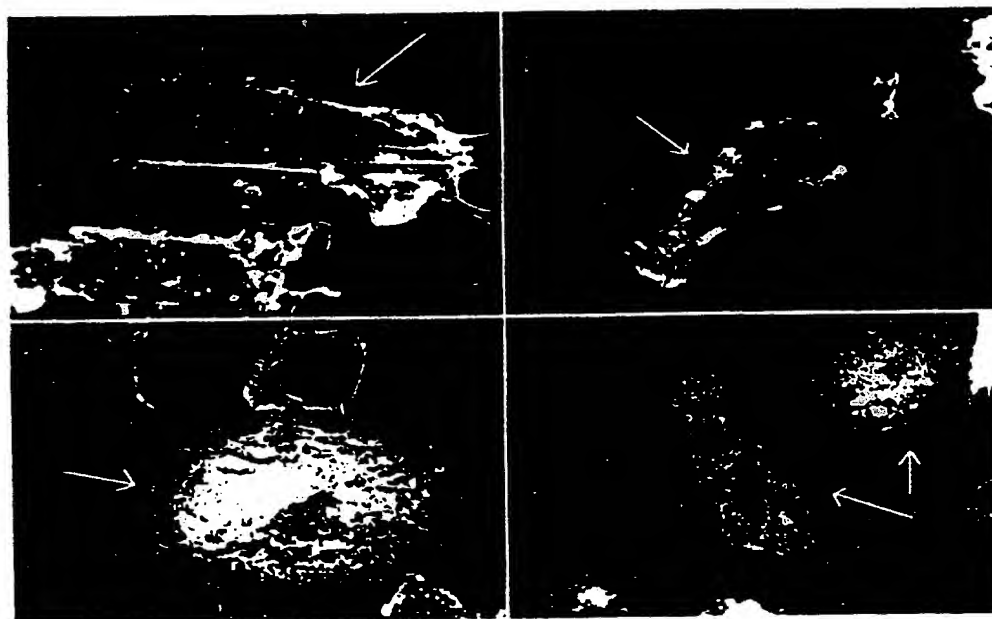
Figure 9 Cont/d

1501 GTGCATGTCA CCGAGGAGGA GCAGCTGCAG CTGCGGGAAA TCCTGGAGCG  
 1551 GCGGGGGTCT GGGGAGCTGT ATGAGCACGA GAAGGACCTG GTGTGGAAGC  
 1601 TCGGGCATGA AGTCCAGGAG CACTTCCCGG AGGCGCTAGC CCGGCTGCTG  
 1651 CTGGTCACCA AGTGAACAA GCATGAGGAT GTGGCCCAAG TCGTCTACCT  
 1701 GCTGTGCTCC TGGCCGGAGC TGGCCCTCCT GAGCGCCCTG GAGCTGCTAG  
 1751 ACTTCAGCTT CCGCGATTGC CACGTAGGCT CCTTCGCCAT CAAGTGGCTG  
 1801 CGGAACCTGA CGGACGATGA GCTGTTCCAG TACCTGCTGC AGCTGGTGCA  
 1851 GGTGCTCAAG TACGAGTCCT ACCTGGACTG CGAGCTGACC AAATTCCTGC  
 1901 TGGACCGGGC CCTGGCCAAC CGCAAGATCG GCCACTTCCT TTTCTGGCAC  
 1951 CTCCGCTCCG AGATGCACGT GCGGTCCGTG GCCCTGCGCT TCGGCTCAT  
 2001 CCTGGAGGCC TACTGCAGGG GCAGGACCCA CCACATGAAG GTCTGATGA  
 2051 AGCAGGGGGA AGCACTGAGC AACTGAAGG CCTGAATGA GTTGTCAAG  
 2101 CTGAGCTCTC AGAAGACCCC CAAGCCCCAG ACCAAGGAGC TGATGCACTT  
 2151 GTGCATGCCG CAGGAGGCTT ACCTAGAGGC CCTCTCCGAC CTTCAGTCCC  
 2201 CACTCGACCC CAGCACCCCTG CTGGCTGAAG TCTGCTGGA GCACTGCACC  
 2251 TTCACTGACT CCAAGATGAA GCGCTGTGG ATCATGTACA GCAACGAGGA  
 2301 GGCAGGCAGC GCGGGCAGCG TGGGCATCAT CTTTAAGAAC GGGATGACC  
 2351 TCGGGCAGGA CATGCTGACC CTGCAGATGA TCCAGCTCAT GGAGCTCCTG  
 2401 TGGAGGCAGG AGGGGCTGGA CCTGAGGATG ACCGCCATAT GGTGCTCCC  
 2451 CACCGGGGAC CCGACAGGCC TCATTGAGGT GGTACTCCCT TCAGACACCA  
 2501 TCGCCAAACAT CCAACTCAAC AAGAGCAACA TGGCAGCCAC AGCTGCTTC  
 2551 AACAGGATG CCTGTCTCA CTGGCTGAAG TCCAAGAAC CCGGGGAGGC  
 2601 CCGTATCGA GGCATTGAGG AGTTCACCT CTCTGTGCT GGTATTGTG  
 2651 TGGCTACATA TGTGCTGGGC ATTGGCGATC GGCACAGCGA CAATATCATG  
 2701 ATCCGAGAGA GTGGGCAGCT GTTCCACAT GATTTTGGCC ACTTCTGGG  
 2751 GAATTTCAAG ACCAAGTTTG GAATCAACCG CGAGCGTGTC CCATTCATCC  
 2801 TCACCTACGA CTTTGTCCAT GTGATTCAGC AGGGGAAGAC TAATAATAGT  
 2851 GAGAAATTTG AACGGTTCCG GGGCTACTGT GAAAGGGCCT ACACCATCCT  
 2901 GCGGGGCCAC GGGCTTCTCT TCCTCCACCT CTTTGGCTTG ATCGGGGGG  
 2951 CAGGCTGCC TGAGCTCAGC TGCTCCAAAG ACATCCAGTA TCTCAAGGAC  
 3001 TCCCTGGCAC TGGGGAAC AGAGGAGGAG GCACTGAAGC ACTTCCGAGT  
 3051 GAAGTTTAAC GAAGCCCTCC GTGAGAGCTG GAAACCAAA GTCACTGGC

## Figure 9 Cont/d

3101 TGGCCCACAA CGTGTCCAAA GACAACAGGC AGTAGTGGCT CCTCCCAGCC  
3151 CTGGGCCCAA GAGGAGGCGG CTGCGGGTCG TGGGGACCAA GCACATTGGT  
3201 CCTAAAGGGG CTGAAGAGCC TGAAGTGCAC CTAACGGGAA AGAACCGACA  
3251 TGGCTGCCTT TTGTTTACAC TGGTTATTTA TTTATGACTT GAAATAGTTT  
3301 AAGGAGCTAA ACAGCCATAA ACGGAAACGC CTCCTTCATG CAGCGGCGGT  
3351 GCTGGGCCCC CCGAGGCTGC ACCTGGCTCT CGGCTGA

Figure 10





# INTERNATIONAL SEARCH REPORT

1st Application No  
PCT/GB 97/01471

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		Relevant to claim No.
Category *	Citation of document, with indication, where appropriate, of the relevant passages	
Y	WO 93 21328 A (LUDWIG INST CANCER RES ;HILES IAN D (GB); FRY MICHAEL J (GB); DHAN) 28 October 1993 cited in the application see page 1 - page 3, line 27	11-19, 21,22
A	see page 5, line 24 - page 6, line 16 see page 7, line 21 - page 8, line 2 see page 21, line 25 - page 22, line 13; figure 12 see page 59; claim 15	1,2, 5-10,27, 28
P,X	--- VANHAESEBROECK B. ET AL.: "p110 delta, a novel phosphoinositide 3-kinase in leukocytes" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES USA, vol. 94, no. 9, 29 April 1997, pages 4330-4335, XP002044005 see the whole document	1-19,27, 28
A	--- VOLINIA S. ET AL.: "A human phosphatidylinositol 3-kinase complex related to the yeast Vps34p-Vps15p protein sorting system" EMBO JOURNAL, vol. 14, no. 14, 1995, pages 3339-3348, XP002044006 cited in the application -----	



# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/GB 97/01471

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9321328 A	28-10-93	AU 3901793 A	18-11-93
		EP 0590126 A	06-04-94
		JP 6510207 T	17-11-94
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